Fig. 1

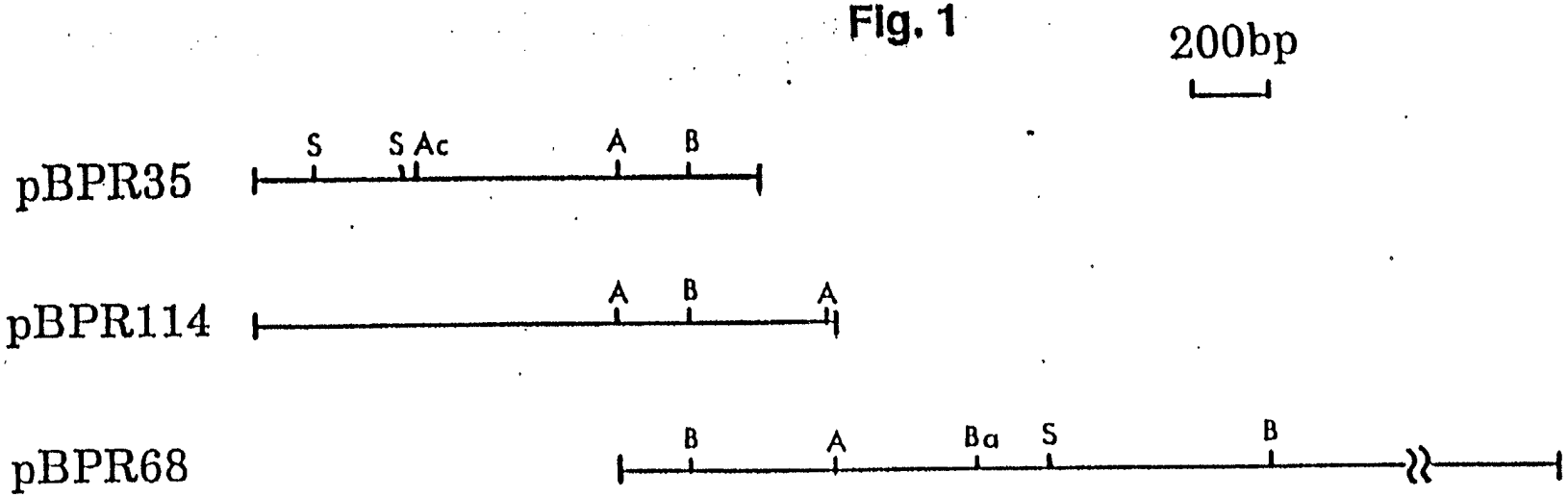

Fig. 2

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184   GCGGCGACTGACAGCGGCGGCGGCGGCGGCAGCGGCTCCAAGGCGAGCGTGGTCCCCGCGTGCGCACAAGCTCGCCGCGCGCGCAGGGACCCA                   275

276   CGGACACCGGGCCCCGGGCGGACACACAGACGCGGAGATCGGGCTCTACGCGCGCTACTCAGCCCACGAGCTCCCCATCCCTGGGCGGAGCGG                   367

368   GGCGCGGACTCGCCGCTGCGCGCCCTCCCCGCGGAGTCTGCCCCGGGCAGACCCGCAGCCCGCGGCCCCCCCCGCGAGGCCCCTGGGTGAGCA                   459

1                                                    Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro Cys Arg              13
460   GCCTGTAGACACCTGGGGTTGAGCAGTGGCGGCTGTGA ATG AGA GGC GGG CGG CAC TGG CCC GAG CCG CCT TGC AGG                   536

14    Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Thr                    36
537   CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC ACC                   605

37    Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn                    59
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60    Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys                    82
675   GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG                   743

83    Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln                   105
744   CCC GCC CAC GTG GGT GAG ATG GTC CTG GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA                   812

106   Val Trp Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met                   128
813   GTC TGG GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG GAT CTC TCA GAC ATG                   881

129   Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys                   151
882   AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT                   950

152   Gly Phe Glu Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr                   174
951   GGG TTT GAG GAG TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG GCC CTG TAC                  1019

175   Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys                   197
1020  ACA GTT GGC TAC AGC ACG TCC CTC GTC ACC GTC ACC ACT GCC ATG GTC ATC CTG TGT CGT TTC CGG AAG                  1088

198   Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val                   220
1089  CTG CAC TGC ACC CGC AAC TTC ATC CAC ATG AAC CTC TTC GTG TCG TTT ATG CTG AGG GCC ATC TCC GTC                  1157

221   Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Val Ser Thr Val Glu Cys                   243
1158  TTC ATC AAA GAC TGG ATC CTC TAT GCT GAG CAG GAC AGC AAT CAC TGC TTT GTC TCC ACT GTG GAA TGC                  1226

244   Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu                   266
1227  AAG GCT GTG ATG GTT TTC TTC CAC TAC TGT GTT GTA TCC AAC TAC TTC TGG CTG TTC ATC GAG GGC CTG                  1295

267   Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile Ile                   289
1296  TAT CTC TTC ACC CTG CTG GTG GAG ACC TTC TTC CCC GAG AGG AGA TAT TTC TAC TGG TAC ATC ATC ATT                  1364

290   Gly Trp Gly Thr Pro Thr Val Cys Val Ser Val Trp Ala Met Leu Arg Leu Tyr Phe Asp Asp Thr Gly                   312
1365  GGC TGG GGG ACA CCA ACT GTG TGT GTG TCT GTG TGG GCT ATG CTG AGG CTC TAC TTC GAT GAC ACA GGC                  1433

313   Cys Trp Asp Met Asn Asp Asn Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met                   335
1434  TGC TGG GAT ATG AAT GAC AAC ACG GCT CTG TGG TGG GTG ATC AAA GGC CCT GTA GTT GGC TCC ATA ATG                  1502

336   Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly                   358
1503  GTT AAT TTT GTG CTC TTC ATC GGC ATC ATT GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA                  1571

359   Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys Pro Gln Arg Ala Gln Gln                   381
1572  GGC AAC GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG CCA CAG CGG GCT CAG CAG                  1640

382   His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile                   404
1641  CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTA CGG CTC GCC AGG TCC ACC TTG CTG CTC ATC                  1709

405   Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu                   427
1710  CCA CTC TTT GGA ATC CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG AGG GAG AGA CTG                  1778

428   Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly                   450
1779  GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAT TGC TTT CTG AAT GGA                  1847

451   Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe                   473
1848  GAG GTG CAG GCG GAG ATC AAG AGG AAG TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG GAC TTC                  1916

474   Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys                   496
1917  AAG CAC CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG                  1985

497   Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr •••                                       513
1986  AGC AGC TCC CAG ATC CGC ATG TCT GGG CTT CCG GCC GAC AAC CTG GCC ACC TGA GCCCACCCTGCCCCCTCCTC                 2059

2060  TCCTCTGTACGCAGGCTGGGGCTGTGGTGGGGCGCCGGCCCACGCATGTTGTGCCTCTTCTCGCCTTCGGGCAGGCCCCGGGCTGGGCGCCT                 2151

2152  GGCCCCCGAGGTTGGAGAAGGATGCGGGACAGGCAGCTGTTTAGGCTTCCTGTTTTGGCGCTGGCCCAACCACCGTGGGTCCCTGGGCCTGC                 2243

2244  ACCCAGACATGTAATACTCGTTAATTGGGAAGTCATCCATTCTTTCGCTTTCGCAAGTCGTTGCTTATTAAGAGGTTCAAGTCACCTACCCA                 2335

2336  ATTCAGAAGCTTAAGTAACCACTAACCACCGTGACTGCGTGGGAGGCCTCCCATGGGCTGAGCTACTGACTTGGCTTTGGGGGCCTTGGGCT                 2427

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2704  GTAGGGCTAAGGCCAGAGAAAAGTTCTGGAGCTTTTCATTTGGCCCAAGAAAAAACTGCCAAGATCCAGAAAAGTGGATCTGAGTGGAATTT                 2795

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Fig. 3

```
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 276  CGGACACGGGCGCCGGCGGACACACAGACGCGGAGATCGGGGTCTACGCGCGCTACTGAGCGCACGAGCTCCCCATCCCTGGCCCGAGCGG     367

 368  GGCGCGGACTCGCCGCTGCGCGGCCTCCCCGCCGAGTGTGCCCCGGGCAGACCCGCAGCCCGCGGCCCCCGCCGCGAGGCCCCTCGGTGAGCA     459

   1                                    Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro Cys Arg      13
 460  GCCTGTAGACACCTGGGGTTGAGCAGTGGCGGCTGTGA ATG AGA GGC GGG CGG CAC TGG CCC GAG CCG CCT TGC AGG      526

  14  Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Thr      38
 527  CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT GCT GTC CTC CTG CTG CCT ATG GCC ACC      605

  37  Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn      59
 606  GCC ATG CAT TCC GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT      674

  60  Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys      82
 675  GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG      743

  83  Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln     105
 744  CCC GCC CAC GTG GGT GAG ATG GTC CTG GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA      812

 106  Val Trp Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met     128
 813  GTC TGG GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG GAT CTC TCA GAC ATG      881

 129  Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys     151
 882  AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT      950

 152  Gly Phe Glu Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr     174
 951  GGG TTT GAG GAG TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG GCC CTG TAC    1019

 175  Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys     197
1020  ACA GTT GGC TAC AGC ACG TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTG TGT CGT TTC CGG AAG    1088

 198  Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val     220
1089  CTG CAC TGC ACC CGC AAC TTC ATC CAC ATG AAC CTC TTC GTG TCG TTT ATG CTG AGG GCC ATC TCC GTC    1157

 221  Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Val Ser Thr Val Glu Cys     243
1158  TTC ATC AAA GAC TGG ATC CTC TAT GCT GAG CAG GAC AGC AAT CAC TGC TTT GTC TCC ACT GTG GAA TGC    1226

 244  Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu     266
1227  AAG GCT GTG ATG GTT TTC TTC CAC TAC TGT GTT GTA TCC AAC TAC TTC TGG CTG TTC ATC GAG GGC CTG    1295

 267  Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile Ile     289
1296  TAT CTC TTC ACC CTG CTG GTG GAG ACC TTC TTC CCC GAG AGG AGA TAT TTC TAC TGG TAC ATC ATC ATT    1364

 290  Gly Trp Gly Thr Pro Thr Val Cys Val Ser Val Trp Ala Met Leu Arg Leu Tyr Phe Asp Asp Thr Gly     312
1365  GGC TGG GGG ACA CCA ACT GTG TGT GTG TCT GTG TGG GCT ATG CTG AGG CTC TAC TTC GAT GAC ACA GGC    1433

 313  Cys Trp Asp Met Asn Asp Asn Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met     335
1434  TGC TGG GAT ATG AAT GAC AAC ACG GCT CTG TGG TGG GTG ATC AAA GGC CCT GTA GTT GGC TCC ATA ATG    1502

 336  Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly     358
1503  GTT AAT TTT GTG CTC TTC ATC GGC ATC ATT GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA    1571

 359  Gly Asn Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile     381
1572  GGC AAC GAG TCC AGC ATC TAC TTA CGG CTC GCC AGG TCC ACC TTG CTG CTC ATC CCA CTC TTT GGA ATC    1640

 382  His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly     404
1641  CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG AGG GAG AGA CTG GTG TTT GAG CTG GGT    1709

 405  Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu     427
1710  CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAT TGC TTT CTG AAT GGA GAG GTG CAG GCG GAG    1778

 428  Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro     450
1779  ATC AAG AGG AAG TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG GAC TTC AAG CAC CGG CAC CCA    1847

 451  Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile     473
1848  TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAG ATC    1916

 474  Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr ***                                           485
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2088  GATCCGGGACAGGCAGGTGTTTAGGCTTCGTGTTTTGGCGCTGGCCCAACCACCGTGGGTCCGTGGGCCTGCACCCAGACATGTAATACTCC    2179

2180  TTAATTGGGAAGTCATCCATTCTTTCCCTTTCCCAAGTCGTTGCTTATTAAGAGGTTCAAGTCACCTACCCAATTCAGAAGCTTAAGTAACC    2271

2272  ACTAACCACCGTGAGTGCGTGGGAGGCCTCCCATGGGCTGAGCTACTGACTTGGCTTTGGGGGCCTTGGGCTGGGGCCCTCGTTAAAGCCCC    2363

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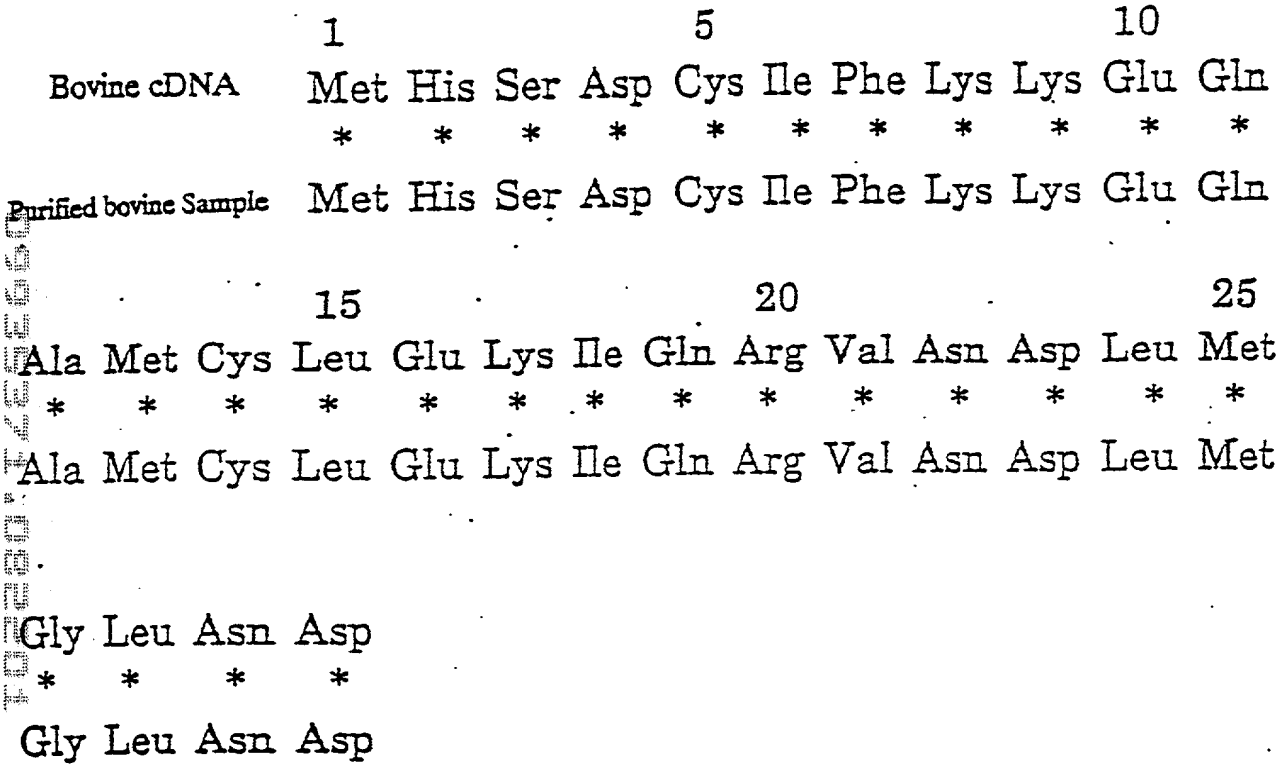
Fig. 4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Purified bovine Sample Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln
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Gly Leu Asn Asp

Fig. 5

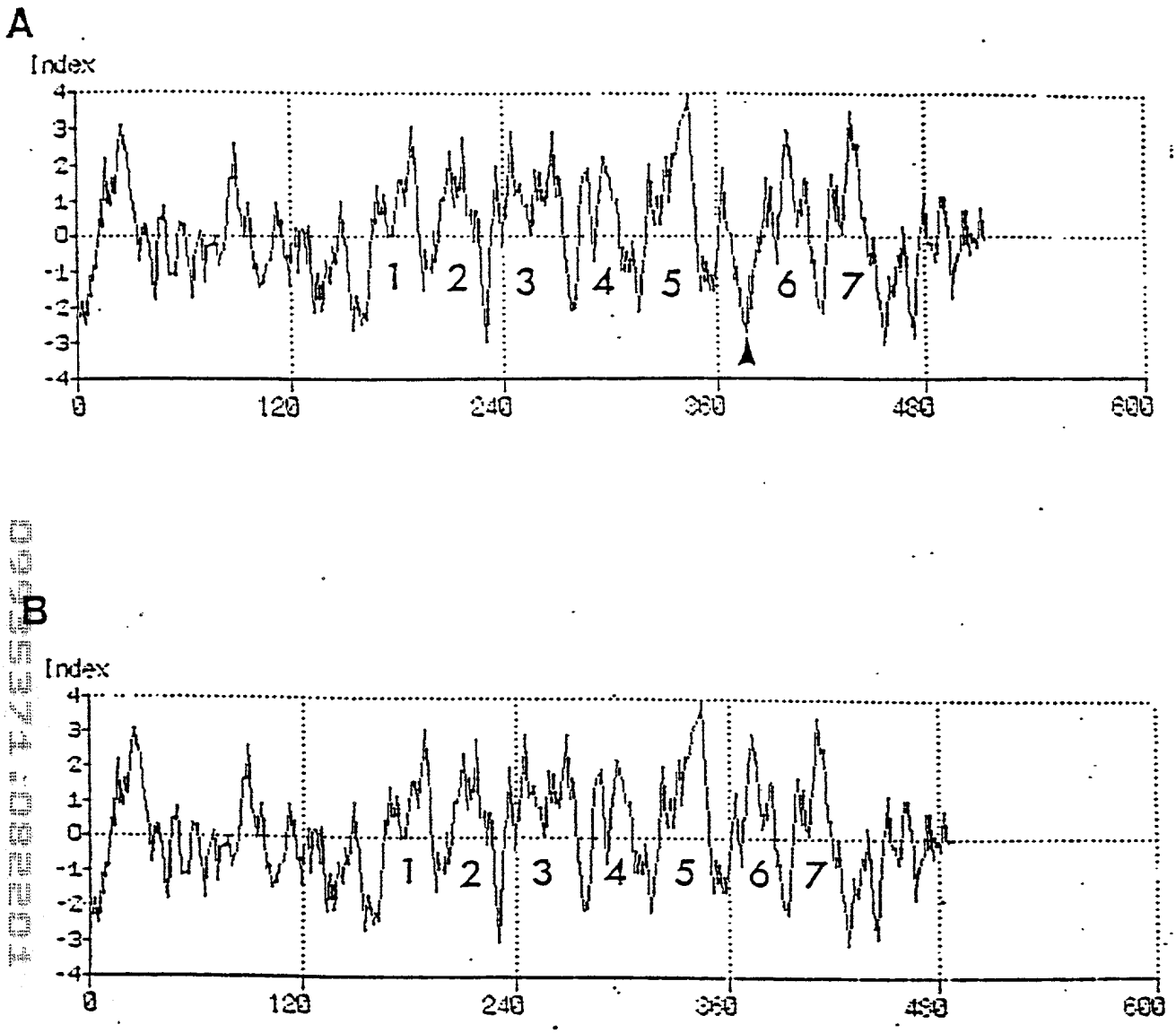
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Fig. 6

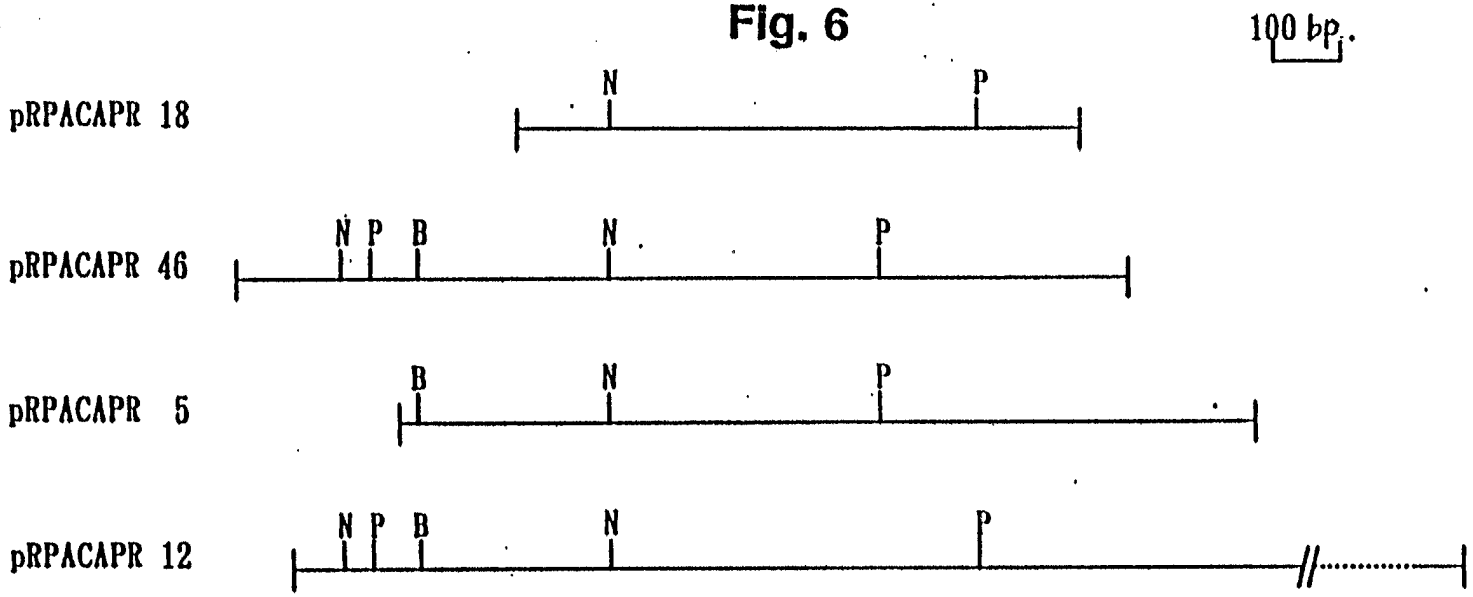

Fig. 7

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 1                      MetAlaArgValLeuGlnLeuSerLeuThrAlaLeuLeuLeu   14

119 CCTGTGGCTATTGCTATGCACTCTGACTGCATCTTCAAGAAGGAGCAAGCCATGTGCCTG  178
 15 ProValAlaIleAlaMetHisSerAspCysIlePheLysLysGluGlnAlaMetCysLeu   34

179 GAGAGGATCCAGAGGGCCAACGACCTGATGGGACTAAACGAGTCTTCCCCAGGTTGCCCT  238
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299 AGCTGCCCTGAGGTCTTCCGGATCTTCAACCCGGACCAAGTCTGGATGACAGAAACCATA  358
 75 SerCysProGluValPheArgIlePheAsnProAspGlnValTrpMetThrGluThrIle   94

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539 CTCTACACAGTCGGCTACAGCACTTCCCTCGCCACCCTCACTACTGCCATGGTCATCTTG  598
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659 TTCATGCTGAGGGCTATCTCCGTCTTCATCAAGGACTGGATCTTGTACGCCGAGCAGGAC  718
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839 GTGGAGACCTTCTTCCCTGAGAGGAGATATTTCTACTGGTACACCATCATCGGCTGGGGG  898
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1079 CAGTCCCCAGACATGGGAGGCAACGAGTCCAGCATCTACTTACGGCTGGCCCGCTCCACC 1138
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```

Fig. 8

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 375 ValSerLysArgGluArgLeuValPheGluLeuGlyLeuGlySerPheGlnGlyPheVal  394

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Fig. 9

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75 SerCysProGluValPheArgIlePheAsnProAspGlnValTrpMetThrGluThrIle 94

359 GGAGATTCTGGTTTTGCCGATAGTAATTCCTTGGAGATCACAGACATGGGGGTCGTGGGC 418
95 GlyAspSerGlyPheAlaAspSerAsnSerLeuGluIleThrAspMetGlyValValGly 114

419 CGGAACTGCACAGAGGACGGCTGGTCGGAGCCCTTCCCCCACTACTTCGATGCTTGTGGG 478
115 ArgAsnCysThrGluAspGlyTrpSerGluProPheProHisTyrPheAspAlaCysGly 134

479 TTTGATGATTATGAGCCTGAGTCTGGAGATCAGGATTATTACTACCTGTCGGTGAAGGCT 538
135 PheAspAspTyrGluProGluSerGlyAspGlnAspTyrTyrTyrLeuSerValLysAla 154

539 CTCTACACAGTCGGCTACAGCACTTCCCTCGCCACCCTCACTACTGCCATGGTCATCTTG 598
155 LeuTyrThrValGlyTyrSerThrSerLeuAlaThrLeuThrThrAlaMetValIleLeu 174

599 TGCCGCTTCCGGAAGCTGCATTGCACTCGCAACTTCATCCACATGAACCTGTTTGTATCC 658
175 CysArgPheArgLysLeuHisCysThrArgAsnPheIleHisMetAsnLeuPheValSer 194

659 TTCATGCTGAGGGCTATCTCCGTCTTCATCAAGGACTGGATCTTGTACGCCGAGCAGGAC 718
195 PheMetLeuArgAlaIleSerValPheIleLysAspTrpIleLeuTyrAlaGluGlnAsp 214

719 AGCAGTCACTGCTTCGTTTCCACCGTGGAGTGCAAAGCTGTCATGGTTTTCTTCCACTAC 778
215 SerSerHisCysPheValSerThrValGluCysLysAlaValMetValPhePheHisTyr 234

779 TGCGTGGTGTCCAACTACTTCTGGCTGTTCATTGAAGGCCTGTACCTCTTTACACTGCTG 838
235 CysValValSerAsnTyrPheTrpLeuPheIleGluGlyLeuTyrLeuPheThrLeuLeu 254

839 GTGGAGACCTTCTTCCCTGAGAGGAGATATTTCTACTGGTACACCATCATCGGCTGGGGG 898
255 ValGluThrPhePheProGluArgArgTyrPheTyrTrpTyrThrIleIleGlyTrpGly 274

899 ACACCTACTGTGTGTGTAACAGTGTGGGCTGTGCTGAGGCTCTATTTTGATGATGCAGGA 958
275 ThrProThrValCysValThrValTrpAlaValLeuArgLeuTyrPheAspAspAlaGly 294

959 TGCTGGGATATGAATGACAGCACAGCTCTGTGGTGGGTGATCAAAGGCCCCGTGGTTGGC 1018
295 CysTrpAspMetAsnAspSerThrAlaLeuTrpTrpValIleLysGlyProValValGly 314

1019 TCTATAATGGTTAACTTTGTGCTTTTCATCGGCATCATCATCATCCTTGTACAGAAGCTG 1078
315 SerIleMetValAsnPheValLeuPheIleGlyIleIleIleIleLeuValGlnLysLeu 334

1079 CAGTCCCCAGACATGGGAGGCAACGAGTCCAGCATCTACTTCAGCTGCGTGCAGAAATGC 1138
335 GlnSerProAspMetGlyGlyAsnGluSerSerIleTyrPheSerCysValGlnLysCys 354

Fig. 10

```
1139 TACTGCAAGCCACAGCGGGCTCAGCAGCACTCTTGCAAGATGTCAGAACTATCCACCATT 1198
 355 TyrCysLysProGlnArgAlaGlnGlnHisSerCysLysMetSerGluLeuSerThrIle  374

1199 ACTCTACGGCTGGCCCGCTCCACCCTACTGCTCATCCCACTCTTCGGAATCCACTACACA 1258
 375 ThrLeuArgLeuAlaArgSerThrLeuLeuLeuIleProLeuPheGlyIleHisTyrThr  394
          △

1259 GTATTCGCCTTCTCTCCAGAGAACGTCAGCAAGAGGGAAAGACTTGTGTTTGAGCTTGGG 1318
 395 ValPheAlaPheSerProGluAsnValSerLysArgGluArgLeuValPheGluLeuGly  414

1319 CTGGGCTCCTTCCAGGGCTTTGTGGTGGCTGTACTCTACTGCTTCCTGAATGGGGAGGTA 1378
 415 LeuGlySerPheGlnGlyPheValValAlaValLeuTyrCysPheLeuAsnGlyGluVal  434

1379 CAGGCAGAGATTAAGAGGAAATGGAGGAGCTGGAAGGTGAACCGTTACTTCACTATGGAC 1438
 435 GlnAlaGluIleLysArgLysTrpArgSerTrpLysValAsnArgTyrPheThrMetAsp  454

1439 TTCAAGCACCGGCACCCGTCCCTGGCCAGCAGTGGAGTAAATGGGGGAACCCAGCTGTCC 1498
 455 PheLysHisArgHisProSerLeuAlaSerSerGlyValAsnGlyGlyThrGlnLeuSer  474

1499 ATCCTGAGCAAGAGCAGCTCCCAGCTCCGCATGTCCAGCCTCCCGGCCGACAACTTGGCC 1558
 475 IleLeuSerLysSerSerSerGlnLeuArgMetSerSerLeuProAlaAspAsnLeuAla  494

1559 ACCTGAGGCCTGTCTCCCTCCTCCTTCTGCACAGGCTGGGGCTGCGGGCCAGTGCCTGAG 1618
 495 Thr***                                                        495

1619 CATGTTTGTGCCTCTCCCCTCTCCTTGGGCAGGCCCTGGGTAGGAAGCTGGGCTCCTCCC 1678
1679 CAAAGGGGAAGAGAGAGATAGGGTATAGGCTGATATTGCTCCTCCTGTTTGGGTCCCACC 1738
1739 TACTGTGATTCATTGAGCCTGATTTGACATGTAAATACACCTCAAATTTGGAAAGTTGCC 1798
1799 CCATCTCTGCCCCCAACCCATGCCCCTGCTCACCTCTGCCAGGCCCCAGCTCAACCTACT 1858
1859 GTGTCAAGGCCAGCCTCAGTGATAGTCTGATCCCAGGTACAAGGCCTTGTGAGCTGAGGC 1918
1919 TGAAAGGCCTGTTTTGGAGAGGCTGGGGTAGTGCCCACCCCAGCAGCCTTTCAGCAAATT 1978
1979 GACTTTGGATGTGGACCCTTCTCAGCCTGTACCAAGTACTGCAGTTGGCTAGGGATGCAG 2038
2039 CTCAGTTTCCTGAGCATCCTTTGGAGCAGGTCAACCTGAGGCTCCTTTTGCTTACCCGAC 2098
2099 ATCTAAGTTGTCCAGGTGCTCGGCTCCTGTGTGCCTGGATGACGGGAGGGCTCCGGGGTC 2158
2159 TTTCAGTCAAAGACTTACATTGAGGTGGGGTGAGAGTCAGAGAAAAGTTCTGGTGCTTTT 2218
2219 CATTTGTTCTAAGAGCTGAGAGCCAGGAATGCAGAGTCAATTGGGAAGGAGATGGGATAG 2278
2279 CTGATGATCTTACCATGTCCATGACTGTGCCCCTGATTCAAGACCGGATCATGTGGTGGC 2338
2339 TTTATTTCTACACTTCTTGTCCACAATGGACAGTCTGAGGAAGCTCTTCTTTCAGCCACA 2398
2399 ACAACCACAGAAAGCCCTTTCTTCTCCCCTCTTGTTTCTCCATAAGTCAAAGCCATGTTT 2458
2459 AGAACGGACCAGCCACCTTGCGATGAAATCACTGAGTTCTGAAGCAACTTTCAATTTCCA 2518
2519 CGAGCCAAGTCCTGGGTCCAGGGACGCCCC                                 2548
```

Fig. 11

Rat	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Bovine	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	1				5					10					15	

Rat	Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu
		*	*	*		*	*	*	*	*	*	*	
Bovine	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp
				20					25				

Fig. 12

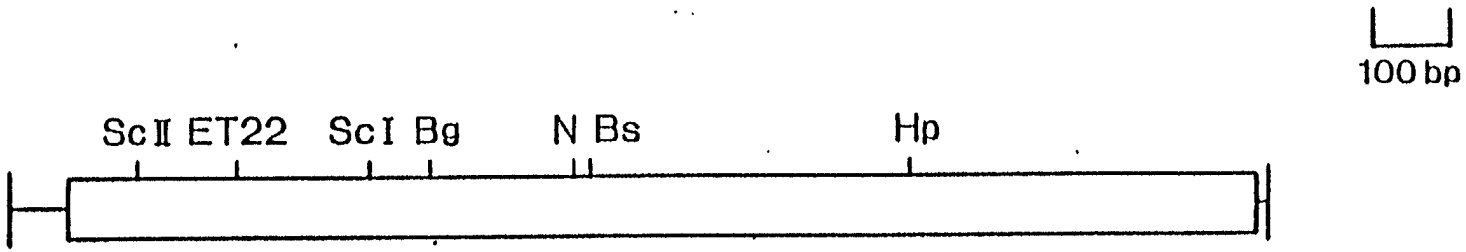

Fig. 13

```
   1    AGCCCAGAGACACATTGGGGCTGACCTGCCGCTGCTGTCAGTGGGAGGCCAGTGGTGCTGGCCAAGAAGTGTC ATG      76
   1                                                                              Met       1

  77  GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC     136
   2  Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly      21

 137  AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC     196
  22  Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp      41

 197  CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC     256
  42  Leu Pro Leu Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val      61

 257  GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC     316
  62  Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp      81

 317  TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG     376
  82  Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu     101

 377  ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG     436
 102  Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp     121

 437  AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC TTC     496
 122  Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe     141

 497  AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC AGT AAC     556
 142  Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser Asn     161

 557  TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG     616
 162  Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser     181

 617  GAA CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG     676
 182  Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly     201

 677  GAC CAG GAT TAT TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC     736
 202  Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser     221

 737  CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA     796
 222  Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr     241

 797  CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC     856
 242  Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe     261

 857  ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC CAC TGC TTC ATC TCC ACT GTG     916
 262  Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val     281

 917  GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC TAC TTC TGG CTG     976
 282  Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu     301

 977  TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG AGA    1036
 302  Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg     321

1037  TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG    1096
 322  Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp     341

1097  GCT ACG CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT    1156
 342  Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala     361

1157  CTG TGG TGG GTG ATC AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT    1216
 362  Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe     381

1217  ATT GGC ATT ATC GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG    1276
 382  Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu     401

1277  TCC AGC ATC TAC TTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC    1336
 402  Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile     421

1337  CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT    1396
 422  His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe     441

1397  GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT    1456
 442  Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn     461

1457  GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC TTC    1516
 462  Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe     481

1517  GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG GGC ACC    1576
 482  Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr     501

1577  CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC    1636
 502  Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp     521

1637  AAT CTG GCC ACC TGA GCCATGCTCCCCT                                                1664
```

Fig. 14

					5					10					15
Human	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Bovine	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu

					20					25				
Human	Glu	Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp	
	*	*	*	*	*		*		*	*	*		*	*	
Bovine	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp	

Fig. 15

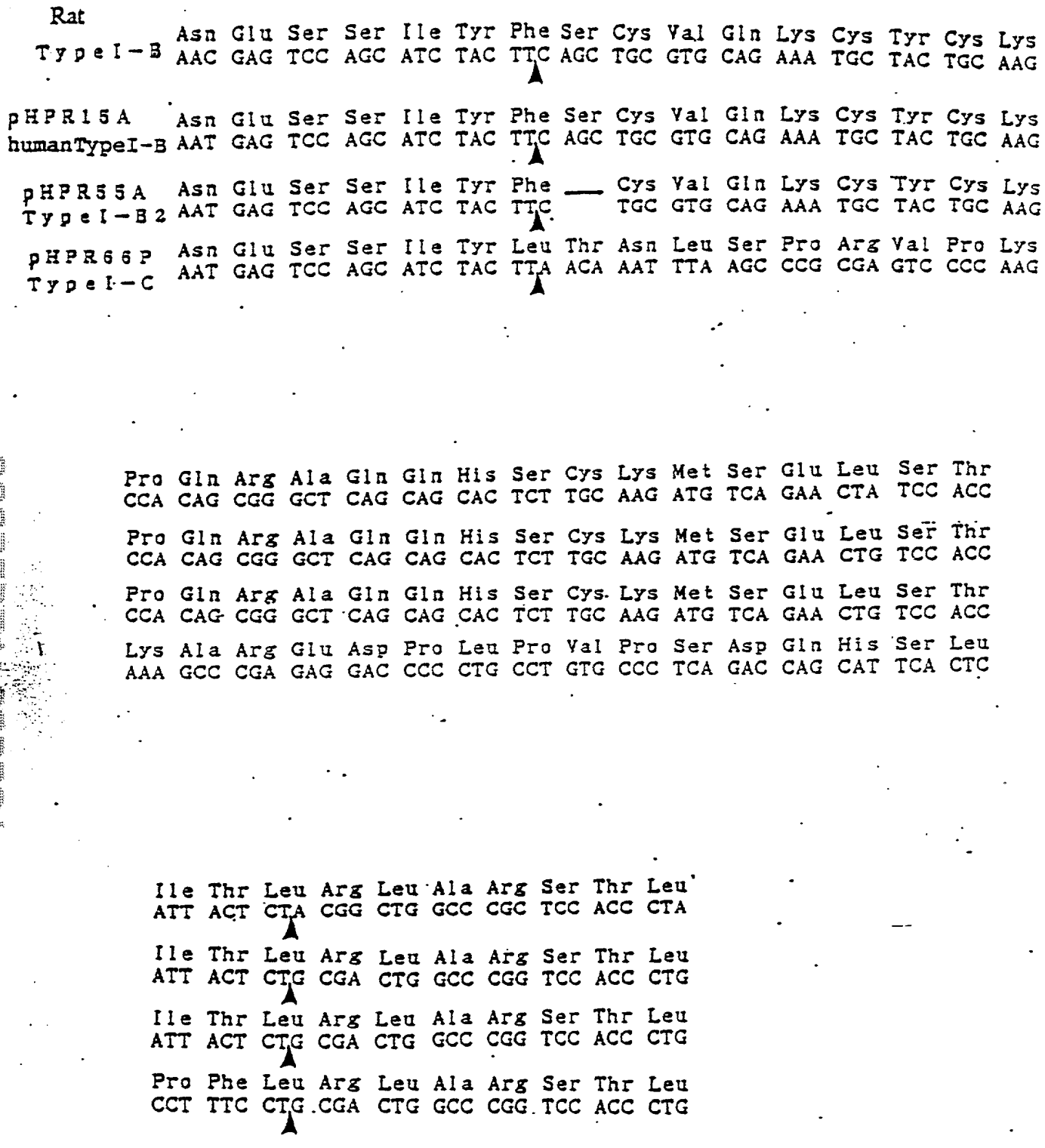
Rat
TypeI-B
Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys
AAC GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG
pHPR15A
humanTypeI-B
Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys
AAT GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG
pHPR55A
TypeI-B2
Asn Glu Ser Ser Ile Tyr Phe — Cys Val Gln Lys Cys Tyr Cys Lys
AAT GAG TCC AGC ATC TAC TTC TGC GTG CAG AAA TGC TAC TGC AAG
pHPR66P
TypeI-C
Asn Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg Val Pro Lys
AAT GAG TCC AGC ATC TAC TTA ACA AAT TTA AGC CCG CGA GTC CCC AAG
Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTA TCC ACC
Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC
Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC
Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln His Ser Leu
AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG CAT TCA CTC
Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTA CGG CTG GCC CGC TCC ACC CTA
Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG
Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG
Pro Phe Leu Arg Leu Ala Arg Ser Thr Leu
CCT TTC CTG CGA CTG GCC CGG TCC ACC CTG

Fig. 16

```
   1     A GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA      67

   1           Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly      21
  68  AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC     136

  22  Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu      44
 137  AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG     205

  45  Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val Ser Leu Ala      67
 206  CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT     274

  68  Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met      90
 275  GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG     343

  91  Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly     113
 344  TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG     412

 114  Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu     136
 413  ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG     481

 137  Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp     159
 482  CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC     550

 160  Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu     182
 551  AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA     619

 183  Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr     205
 620  CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT TAT     688

 206  Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala     228
 689  TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC CTC GTC ACC CTC ACC ACT GCC     757

 229  Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val     251
 758  ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG     826

 252  Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn     274
 827  TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC     895

 275  His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn     297
 896  CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC     964

 298  Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg     320
 965  TAC TTC TGG CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG    1033

 321  Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr     343
1034  AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG    1102

 344  Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile     366
1103  CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG GTG ATC    1171

 367  Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val     389
1172  AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT ATT GGC ATT ATC GTC ATC CTT GTG    1240

 390  Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys     412
1241  CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC    1309

 413  Tyr Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg     435
1310  TAC TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTG CGA    1378

 436  Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro     458
1379  CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA    1447

 459  Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val-     481
1448  GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG    1516

 482  Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys     504
1517  GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG    1585

 505  Val Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly     527
1586  GTG AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG    1654

 528  Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn     550
1655  GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT    1723

 551  Leu Ala Thr ***                                                                               553
1724  CTG GCC ACC TGA GCC ATG CTC CCC T                                                            1748
```

Fig. 17

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1     A GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA      67

1           Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly      21
68  AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC     136

22  Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu      44
137 AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG     205

45  Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val Ser Leu Ala      67
206 CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT     274

68  Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met      90
275 GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG     343

91  Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly     113
344 TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG     412

114 Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu     136
413 ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG     481

137 Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp     159
482 CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC     550

160 Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu     182
551 AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA     619

183 Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr     205
620 CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT TAT     688

206 Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala     228
689 TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC CTC GTC ACC CTC ACC ACT GCC     757

229 Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val     251
758 ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG     826

252 Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn     274
827 TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC     895

275 His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn     297
896 CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC     964

298 Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg     320
965 TAC TTC TGG CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG    1033

321 Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr     343
034 AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG    1102

344 Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile     366
103 CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG GTG ATC    1171

367 Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val     389
172 AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT ATT GGC ATT ATC GTC ATC CTT GTG    1240

390 Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Cys Val Gln Lys Cys Tyr     412
241 CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG TCC AGC ATC TAC TTC TGC GTG CAG AAA TGC TAC    1309

413 Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu     435
310 TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTG CGA CTG    1378

436 Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu     458
379 GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG    1447

459 Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala     481
448 AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT    1516

482 Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val     504
517 GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG    1585

505 Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly     527
586 AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG GGC    1654

528 Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu     550
655 ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG    1723

                                                                                                  552
551 Ala Thr *** .                                                                                1745
724 GCC ACC TGA GCC ATG CTC CCC T
```

Fig. 18

```
   1    A GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG GTG GTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA   67

   1          Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly   21
  68 AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC  136

  22 Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu   44
 137 AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG  205

  45 Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val Ser Leu Ala   67
 206 CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT  274

  68 Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met   90
 275 GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG  343

  91 Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly  113
 344 TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG  412

 114 Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu  136
 413 ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG  481

 137 Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp  159
 482 CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG GAG ACG GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC  550

 160 Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu  182
 551 AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA  619

 183 Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr  205
 620 CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT TAT  688

 206 Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala  228
 689 TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC CTC GTC ACC CTC ACC ACT GCC  757

 229 Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val  251
 758 ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG  826

 252 Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn  274
 827 TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC  895

 275 His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn  297
 896 CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC  964

 298 Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg  320
 965 TAC TTC TGG CTG TTC ATC GAG GGC GTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG 1033

 321 Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr  343
1034 AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG 1102

 344 Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile  366
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1172 AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT ATT GGC ATT ATC GTC ATC CTT GTG 1240

 390 Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg  412
1241 CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG TCC AGC ATC TAC TTA ACA AAT TTA AGC CCG CGA 1309

 413 Val Pro Lys Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln His Ser Leu Pro Phe Leu Arg  435
1310 GTC CCC AAG AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG CAT TCA CTC CCT TTC CTG CGA 1378

 436 Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro  458
1379 CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA 1447

 459 Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val  481
1448 GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG 1516

 482 Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys  504
1517 GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG 1585

 505 Val Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly  527
1586 GTG AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG 1654

 528 Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn  550
1655 GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT 1723

 551 Leu Ala Thr ***                                                                            553
1724 CTG GCC ACC TGA GCC ATG CTC CGC T                                                         1748
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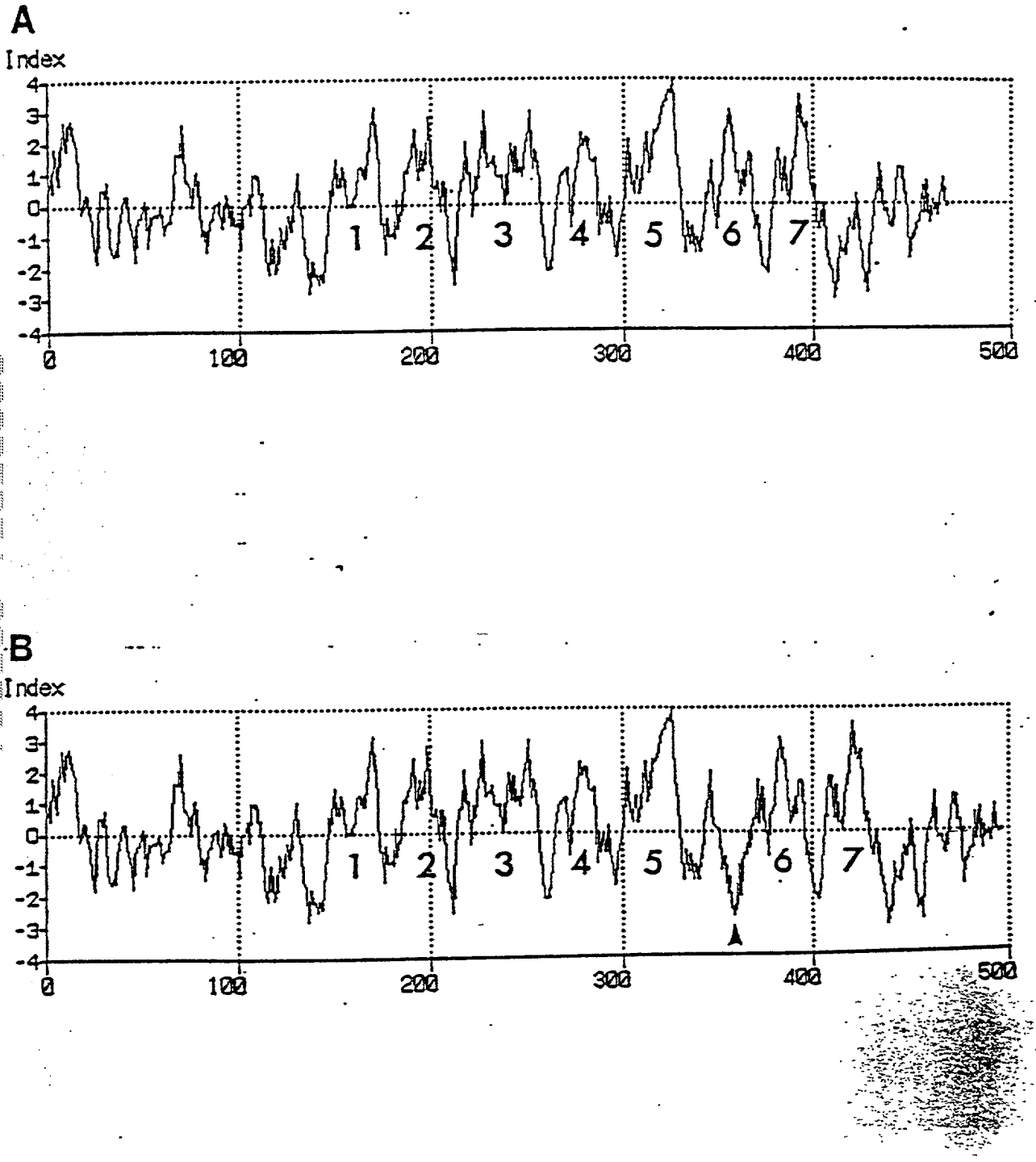
Fig. 19


A
Index
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3
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0
-1
-2
-3
-4
1
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3
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5
6
7
0
100
200
300
400
500
B
Index
4
3
2
1
0
-1
-2
-3
-4
1
2
3
4
5
6
7
0
100
200
300
400
500

Fig. 20

```
EQUIVALENT
   1 : Ala(A),Ser(S),Thr(T),Pro(P),Gly(G)
   2 : Asn(N),Asp(D),Asx(B),Glu(E),Gln(Q),Glx(Z)
   3 : His(H),Arg(R),Lys(K)
   4 : Met(M),Leu(L),Ile(I),Val(V)
   5 : Phe(F),Tyr(Y),Trp(W)

PACAP receptor (upper lines)

VIP   receptor (lower lines)

        19        29        39        49        59        69        79
TALLLPVAIAMHSDCIFKKEQAMCLERIQRANDLMGLNESSPGCPGMWDNITCWKPAQVGEMVLVSCPEV
     *  *              **     * *       *           * *       * *       **
MRPPSPPHVRWLCVLAGALACALRPAGSQAASPQHECEYLQLIEIQRQQCLEEAQLENETTGCSKMWDNL
        10        20        30        40        50        60        70

        89        99       109       119       129       139       149
FRIFNPDQVWMTETIGDSGFADSNSLEITDMGVVGRNCTEDGWSEPFPHYFDACGFDDYEPESGDQDYYY
     *              *    **   ***    * *      *  *   *         *  **  **
TCWPTTPRGQAVVLDCPLIFQLFAPIHGYNISRSCTEEGWSQLEPGPYHIACGLNDRASSLDEQQQTKFY
        80        90       100       110       120       130       140

       159       169       179       189       199       209       219
LSVKALYTVGYSTSLATLTTAMVILCRFRKLHCTRNFIHMNLFVSFMLRAISVFIKDWILYAEQDSSHCF
 **** ****** *****  ** **  ************ ********* ******  **   *  **
NTVKTGYTIGYSLSLASLLVAMAILSLFRKLHCTRNYIHMHLFMSFILRATAVFIKDMALFNSGEIDHCS
       150       160       170       180       190       200       210

       229       239       249       259       269       279       289
VSTVECKAVMVFFHYCVVSNYFWLFIEGLYLFTLLVETFFPERRYFYWYTIIGWGTPTVCVTVWAVLRLY
 *** *** **** ********** **********  ********** * ***** *** **********
EASVGCKAAVVFFQYCVMANFFWLLVEGLYLYTLLAVSFFSERKYFWGYILIGWGVPSVFITIWTVVRIY
       220       230       240       250       260       270       280

       299       309       319       329       339       349       359
FDDAGCWDMNDSTALWWVIKGPVVGSIMVNFVLFIGIIIILVQKLQSPDMGGNESSIYLRLARSTLLLIP
*** ****    ************ ********** ** ****** ***** **** * ***********
FEDFGCWDTIINSSLWWIIKAPILLSILVNFVLFICIIRILVQKLRPPDIGKNDSSPYSRLAKSTLLLIP
       290       300       310       320       330       340       350

       369       379       389       399       409       419       429
LFGIHYTVFAFSPENVSKRERLVFELGLGSFQGFVVAVLYCFLNGEVQAEIKRKWRSWKVNRYFTMDFKH
****** **** ***     ****** ****************************** ****   *   *
LFGIHYVMFAFFPDNFKAQVKMVFELVVGSFQGFVVAILYCFLNGEVQAELRRKWRRWHLQGVLGWSSKS
       360       370       380       390       400       410       420

       439       449       459
RHPSLASSGVNGGTQLSILSKSSSQLRMSSLPADNLAT*
 **  ** *   ********* **  * **    ***
QHPWGGSNGATCSTQVSMLTRVSPSARRSSSFQAEVSLV
       430       440       450
```

Fig. 21

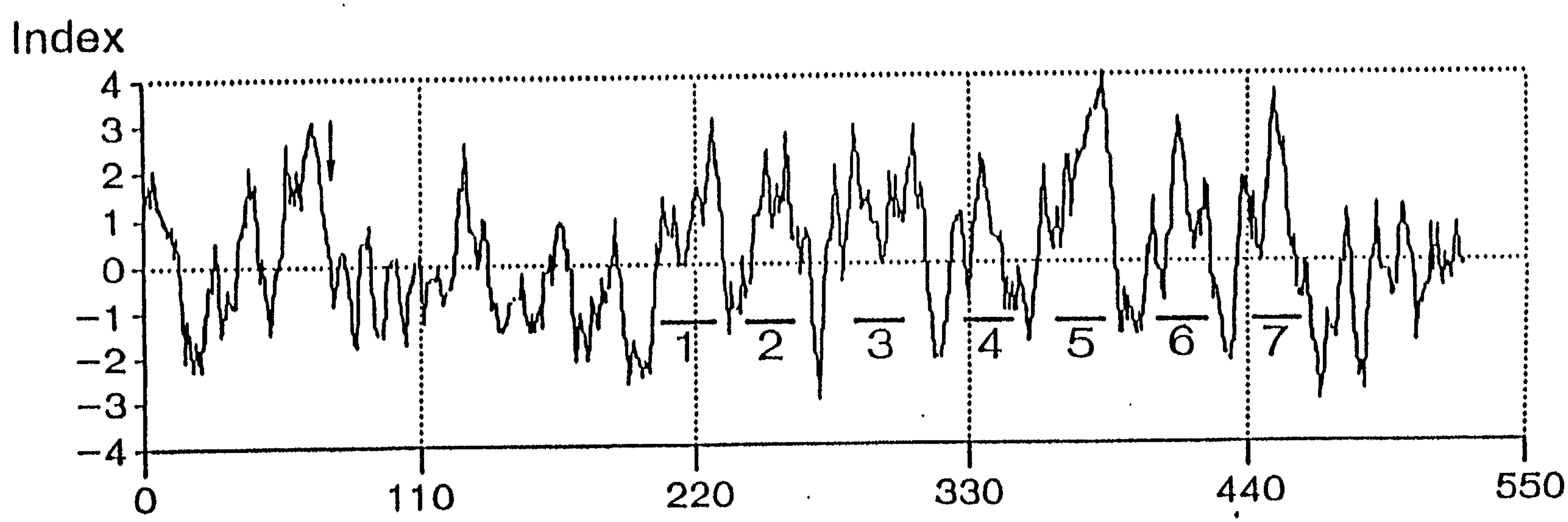


Fig. 22

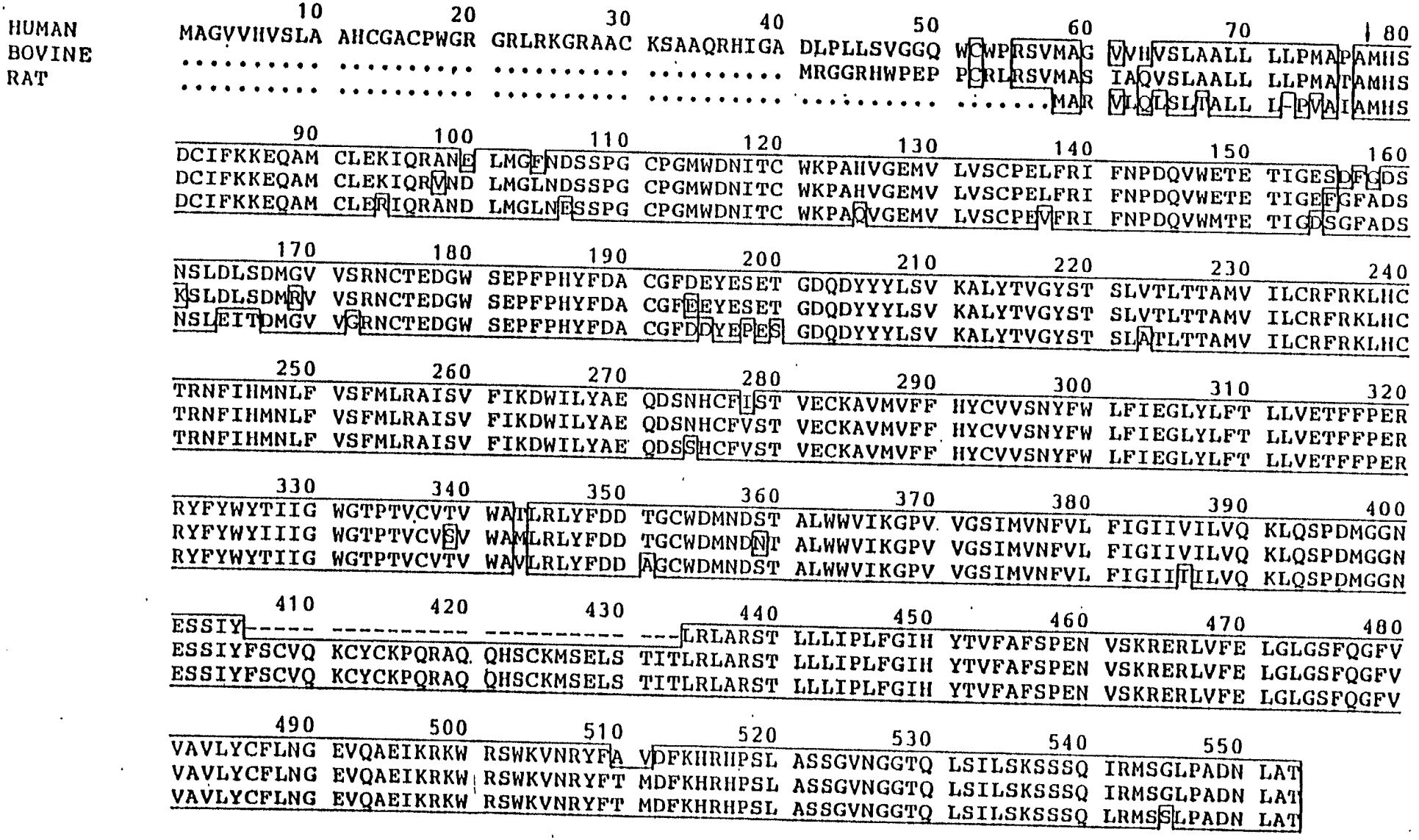


Fig. 23

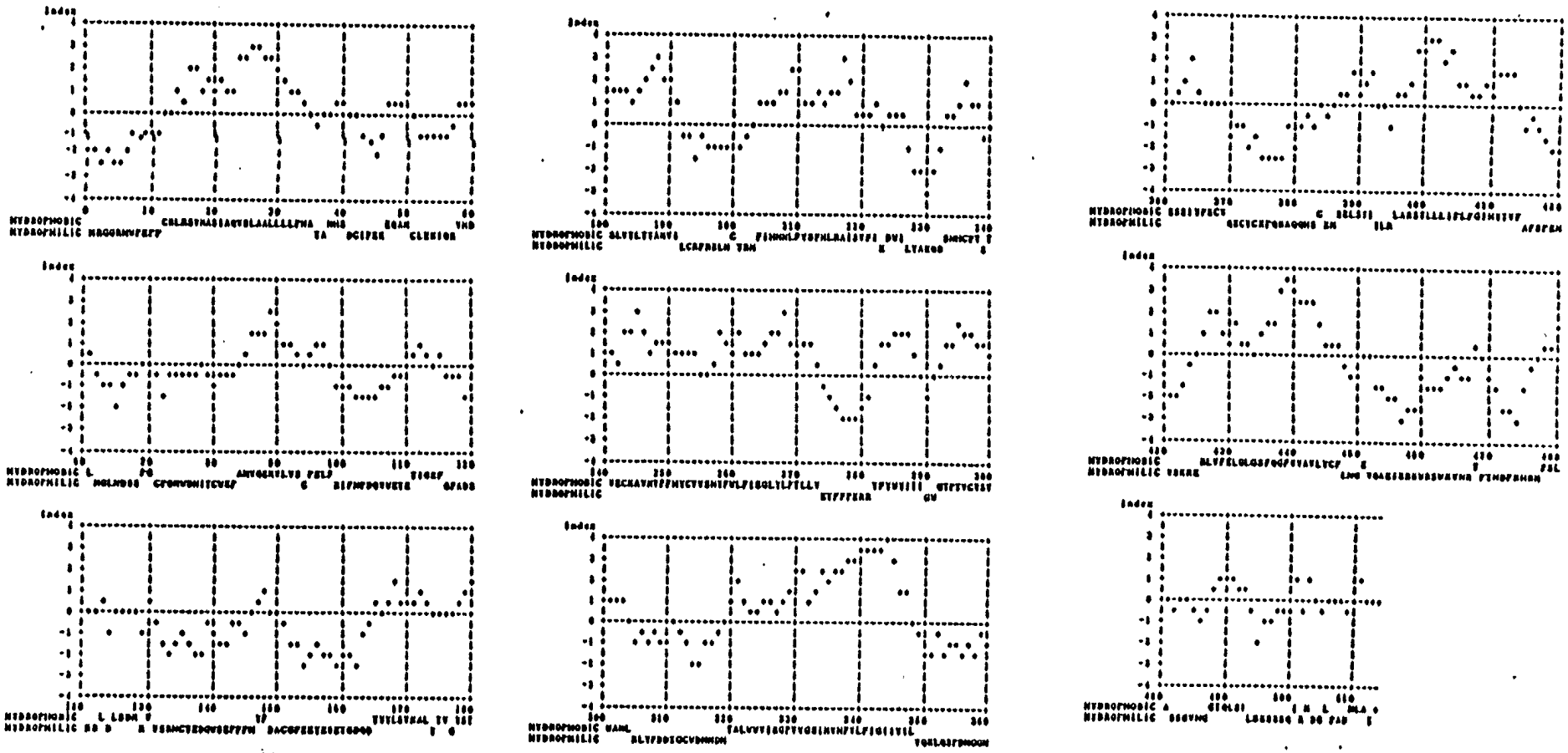


Fig. 24

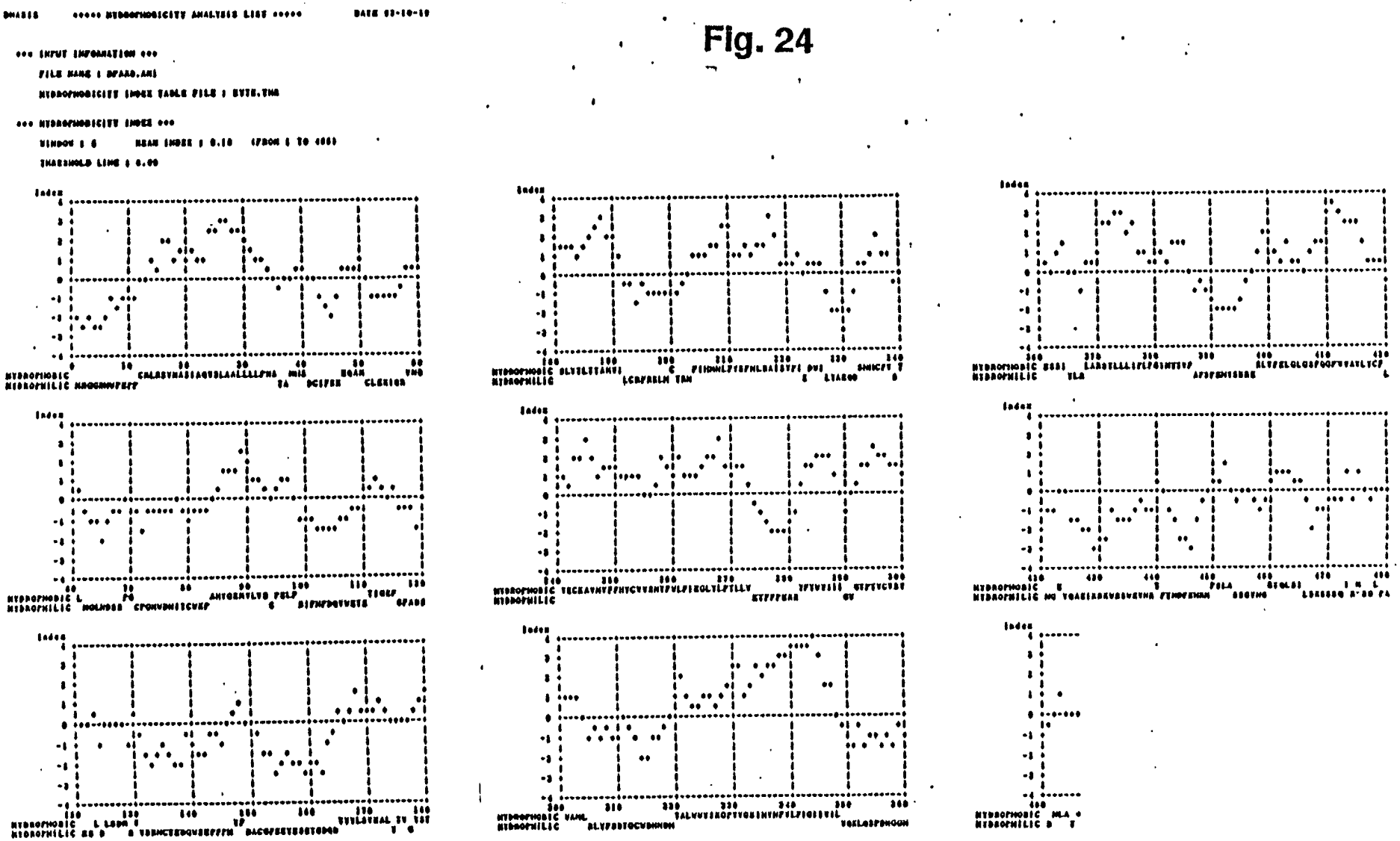


Fig. 25

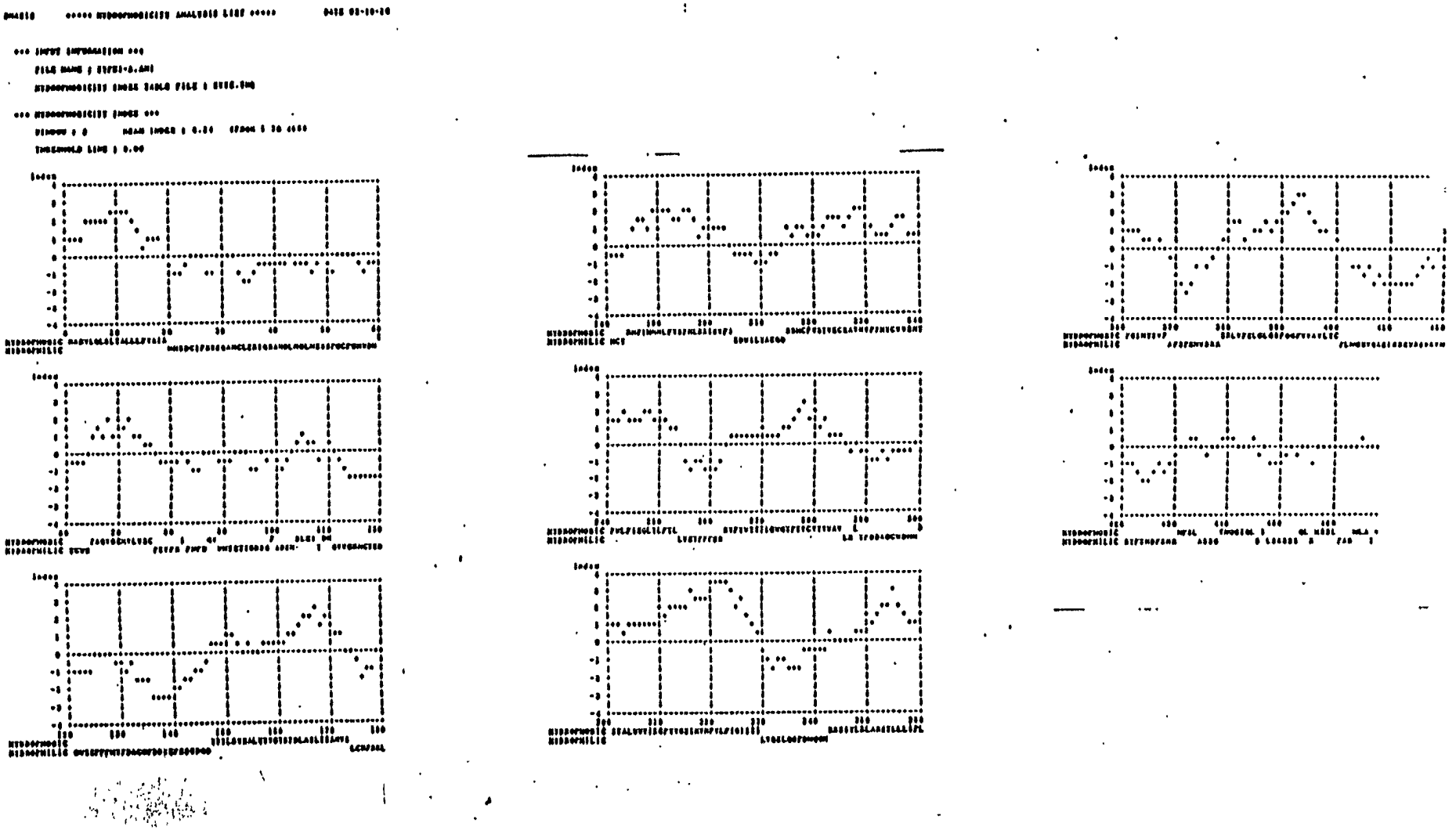


Fig. 26

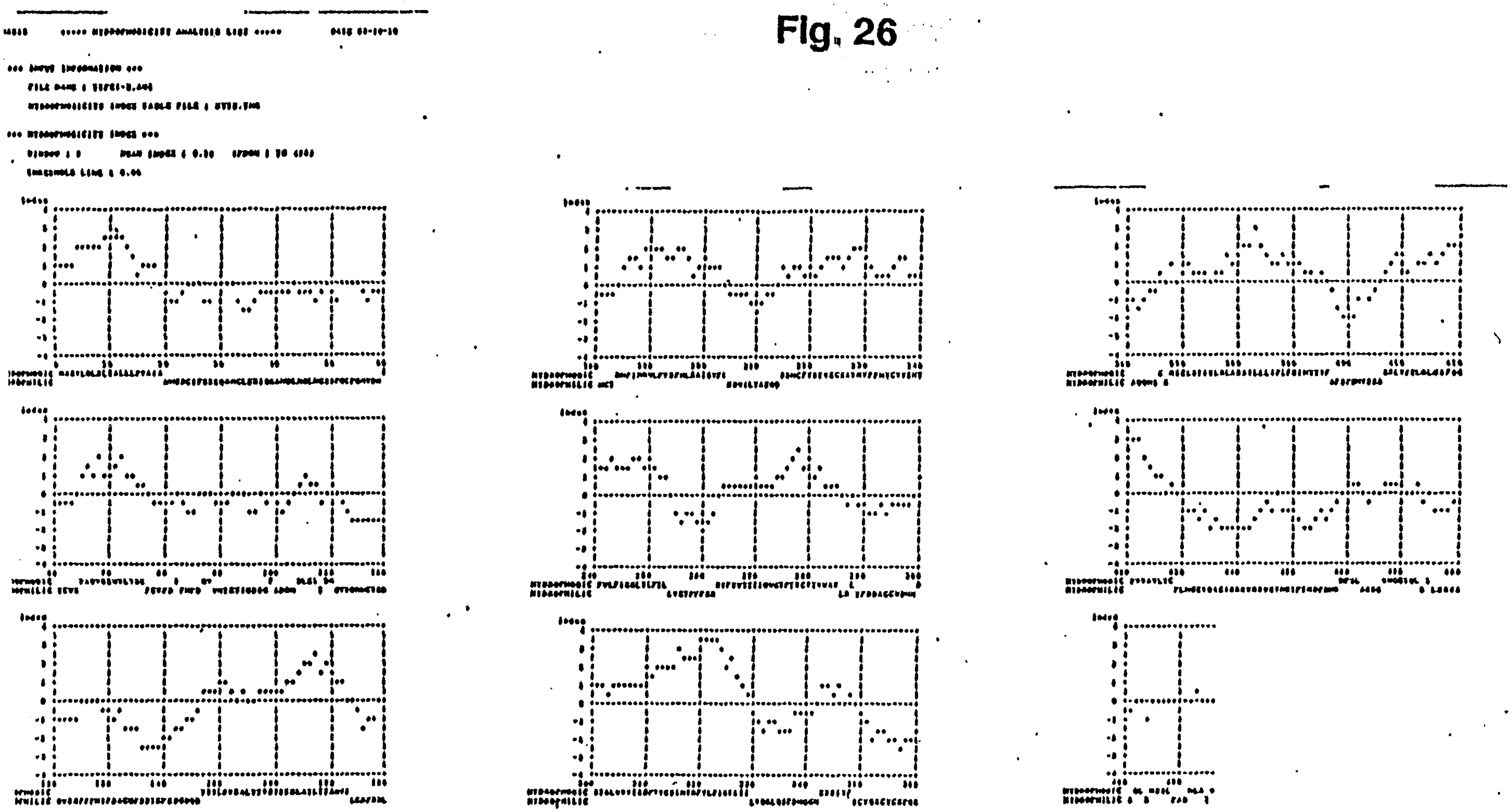


Fig. 27

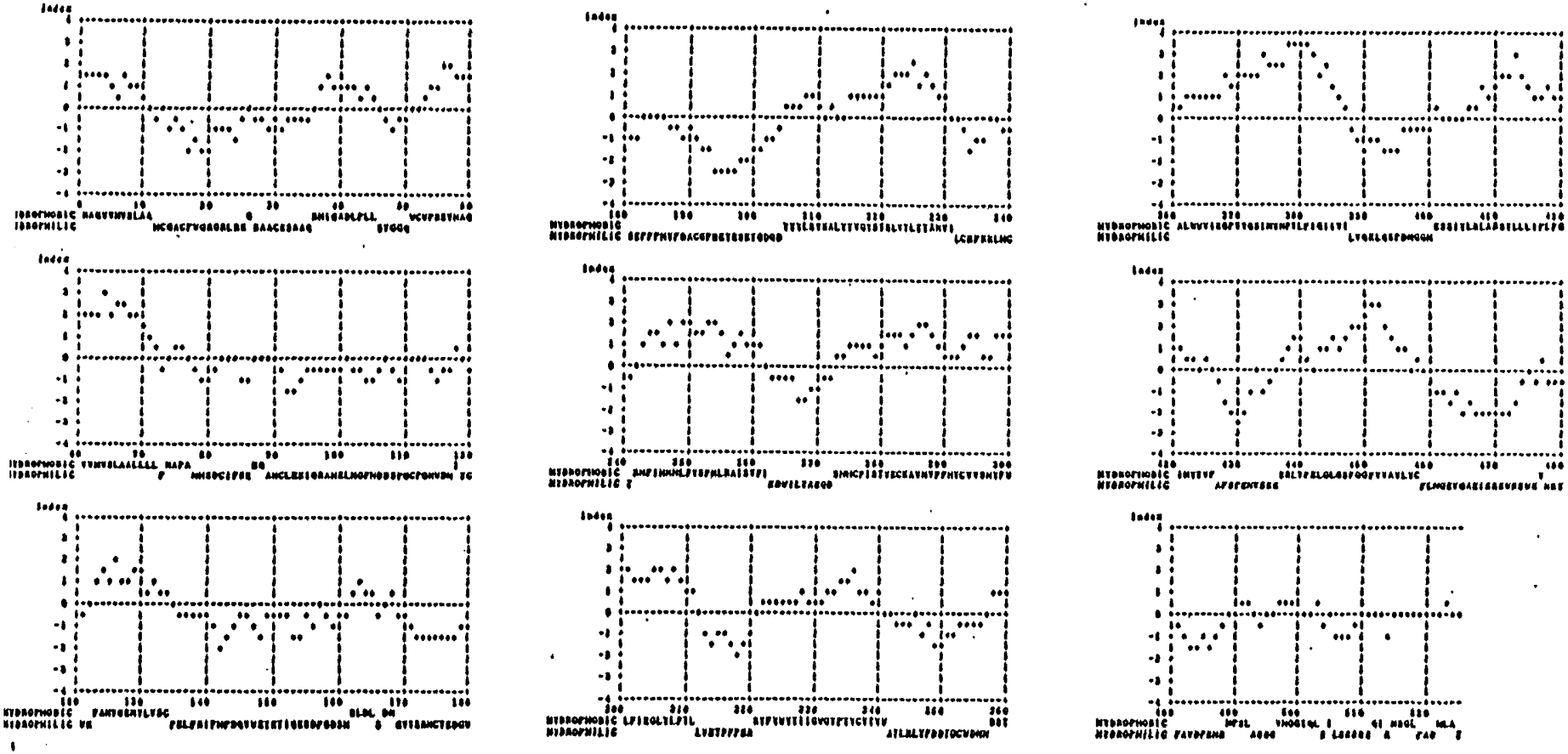

***** HYDROPHOBICITY ANALYSIS LIST *****
*** INPUT INFORMATION ***
*** HYDROPHOBICITY INDEX ***
WINDOW : 9
THRESHOLD LINE : 0.00
Index
HYDROPHOBIC
HYDROPHILIC

Fig. 28

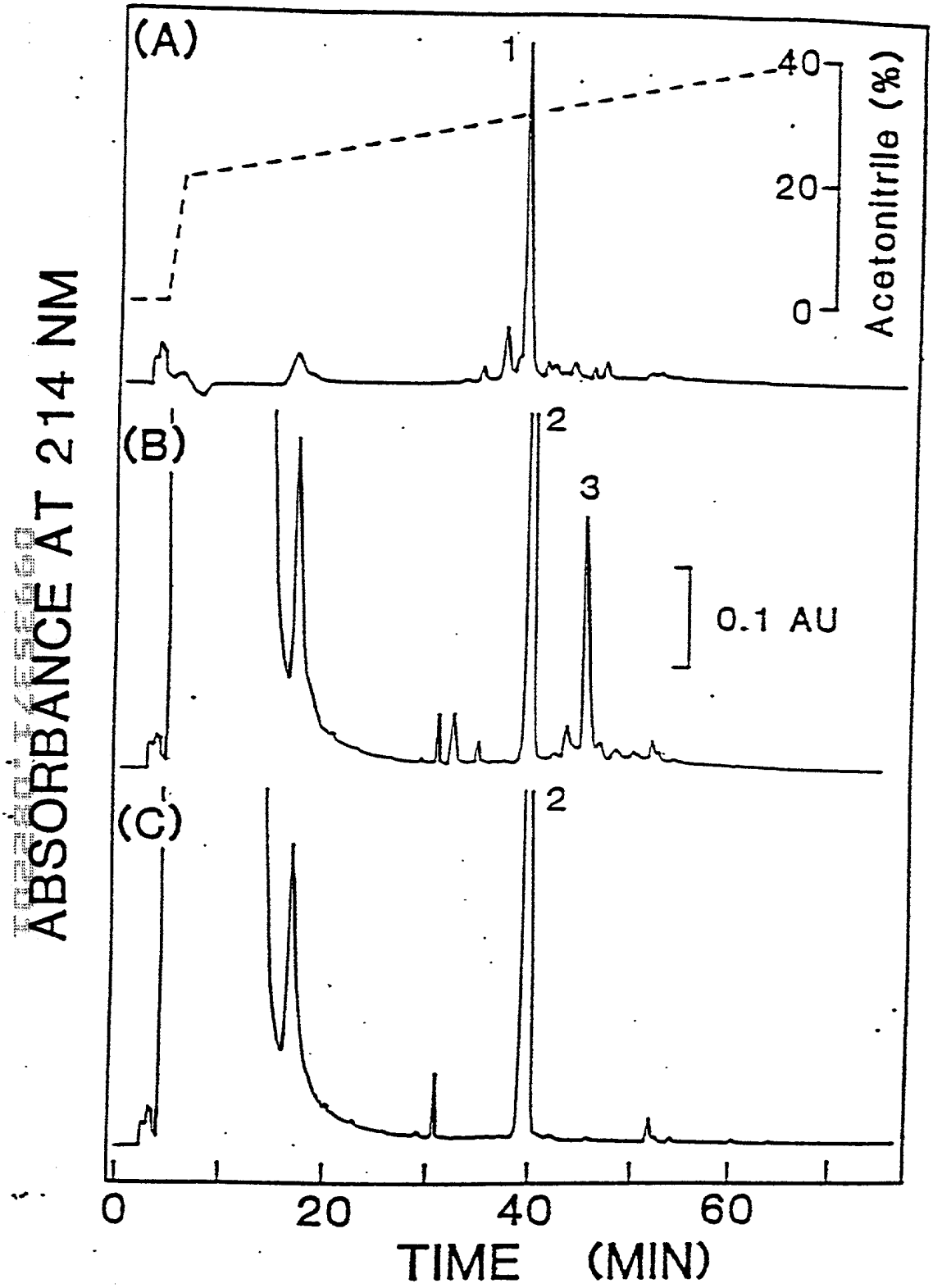

(A)
1
40
20
0
Acetonitrile (%)
(B)
2
3
0.1 AU
(C)
2
ABSORBANCE AT 214 NM
0
20
40
60
TIME (MIN)

Fig. 29

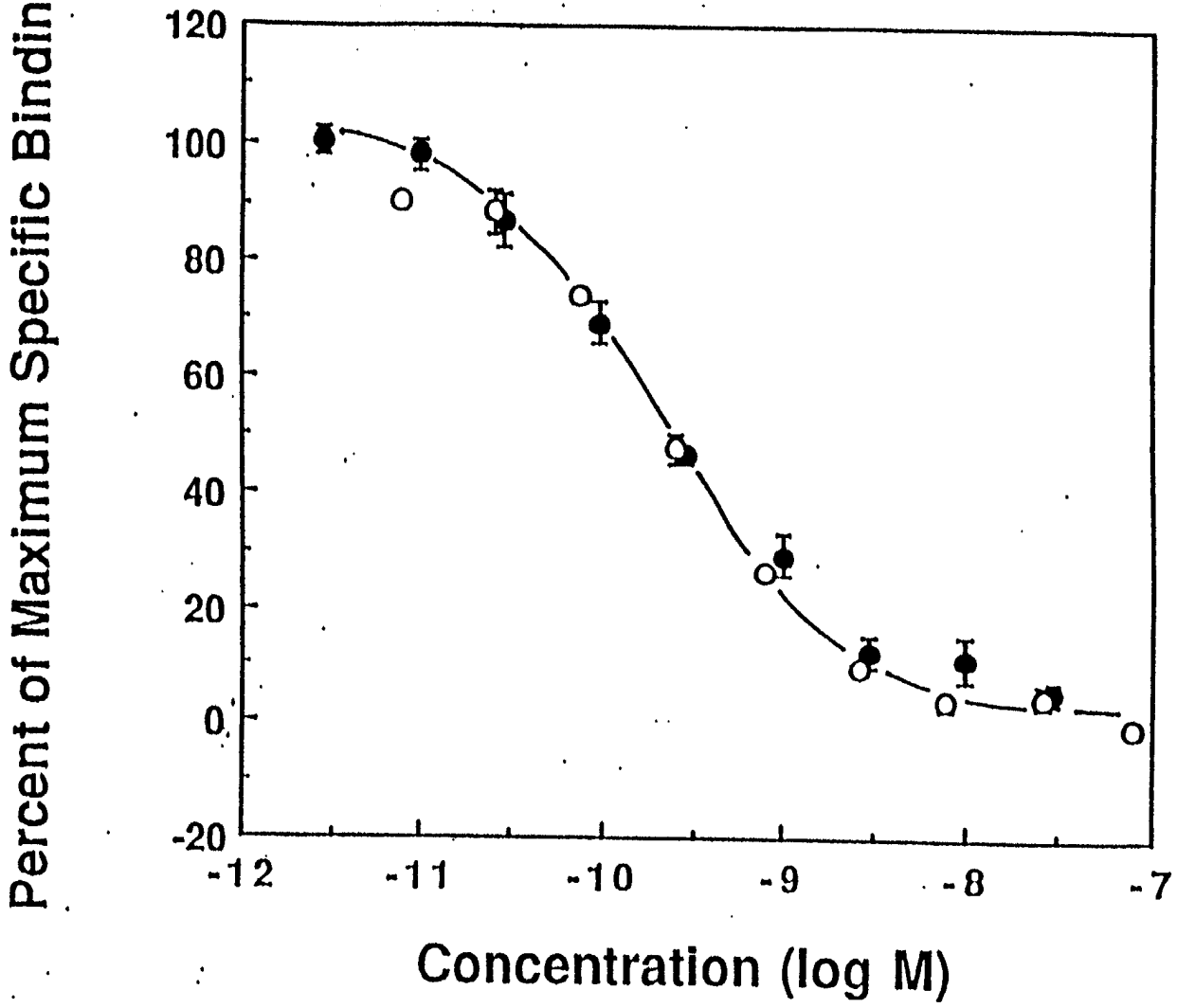


Fig. 30

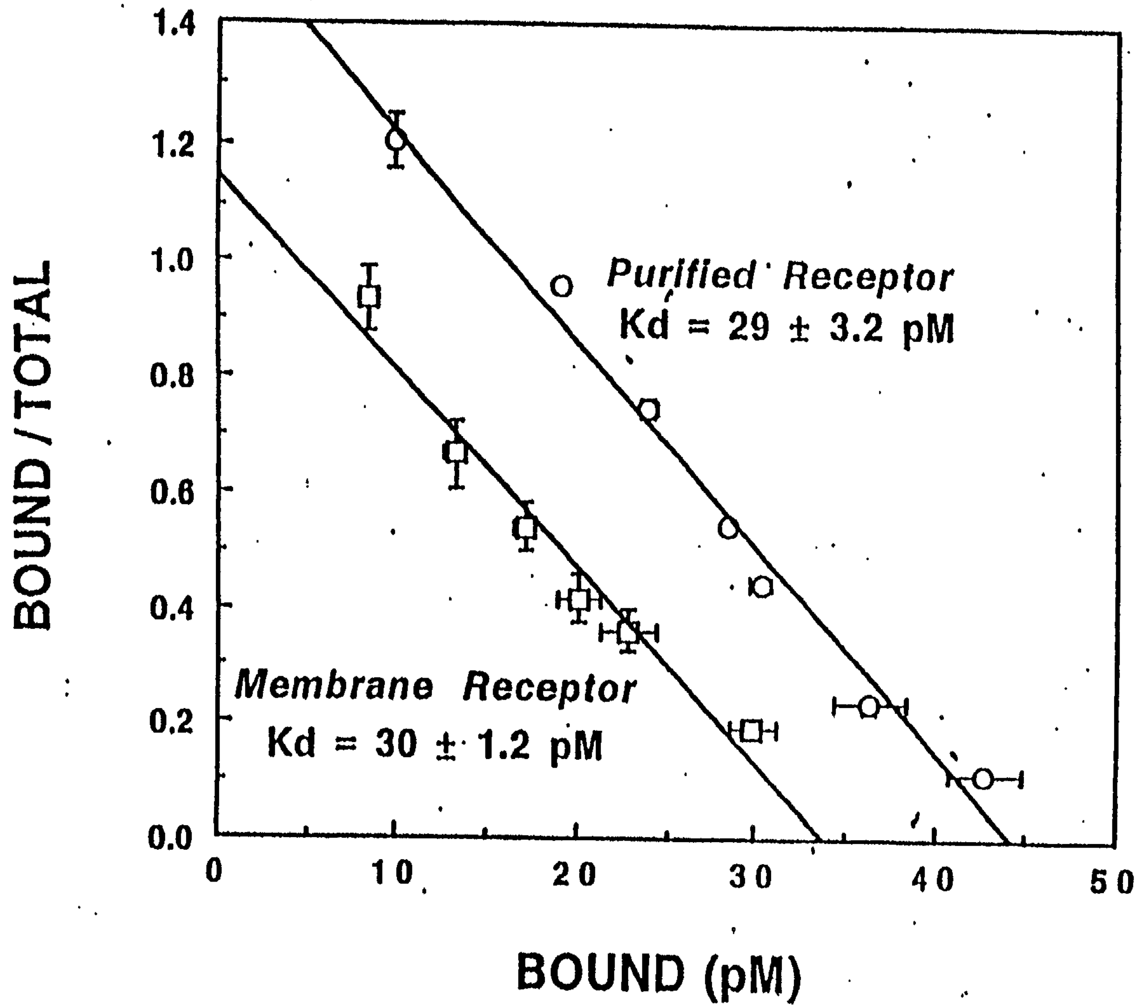

Purified Receptor
Kd = 29 ± 3.2 pM
Membrane Receptor
Kd = 30 ± 1.2 pM
BOUND / TOTAL
BOUND (pM)
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50

Fig. 31

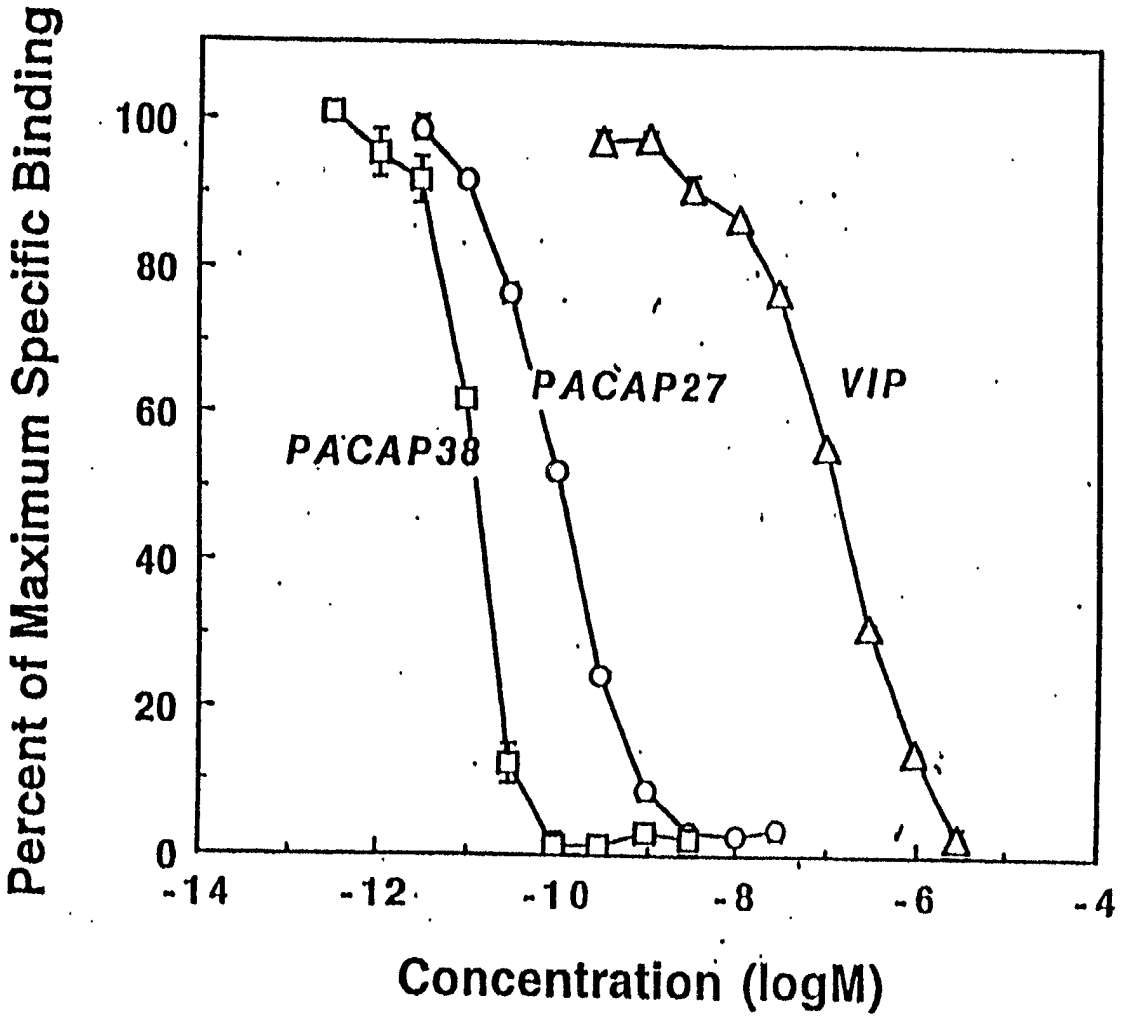


Fig. 32

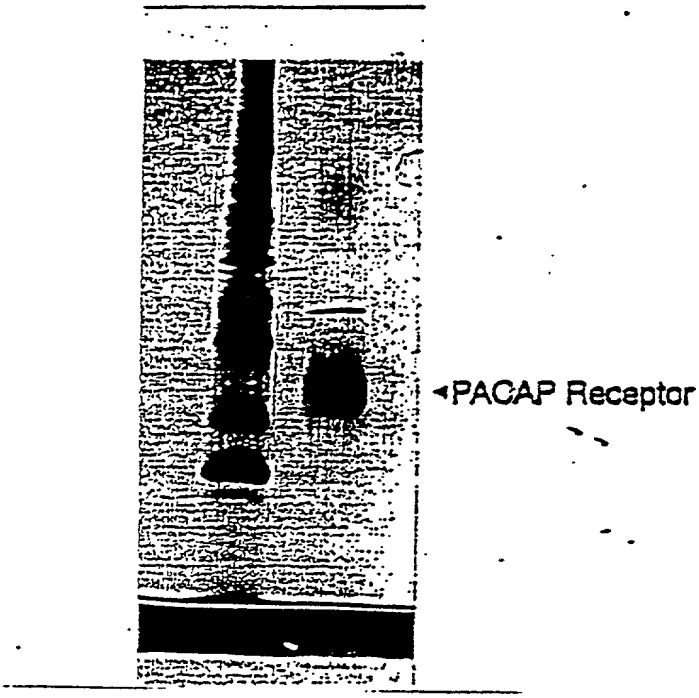


Fig. 33

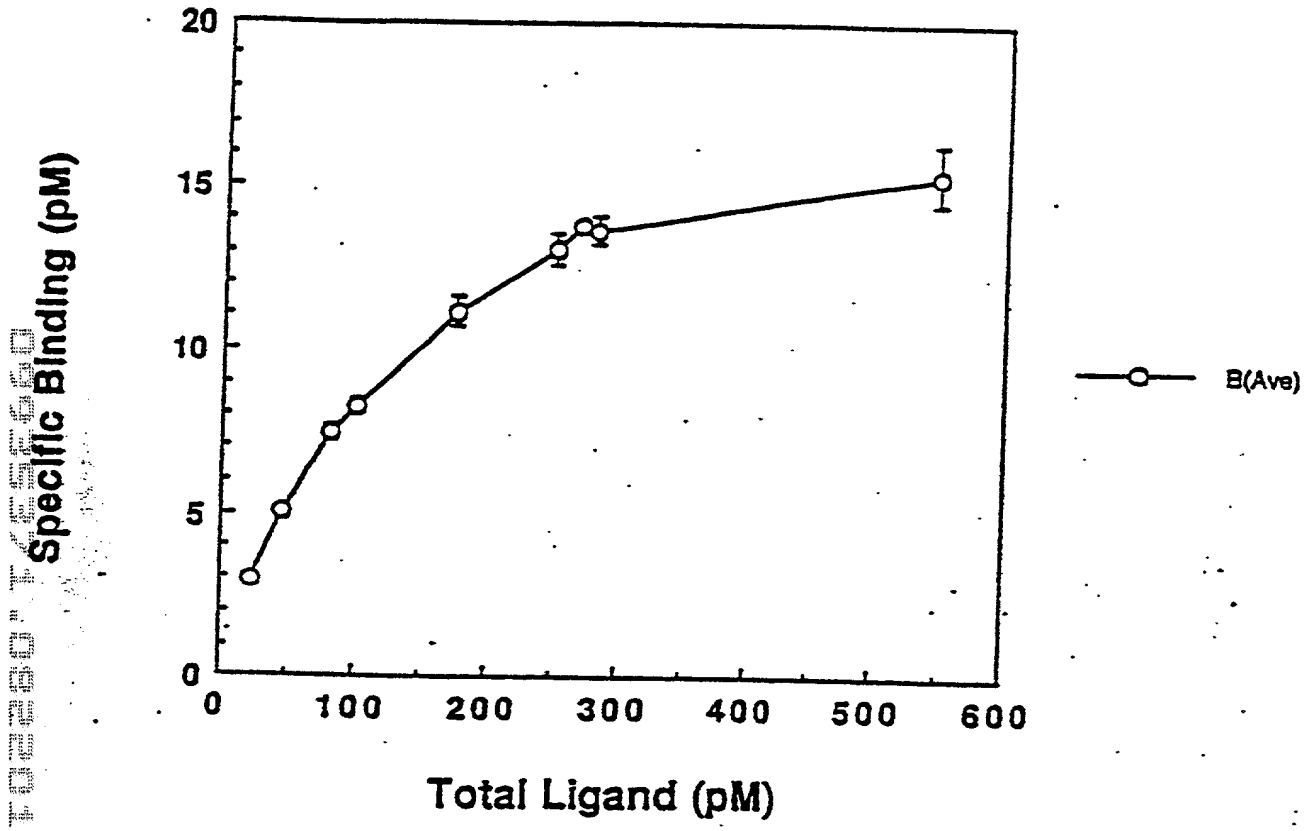

20
15
10
5
0
0
100
200
300
400
500
600
Specific Binding (pM)
Total Ligand (pM)
B(Ave)

Fig. 34

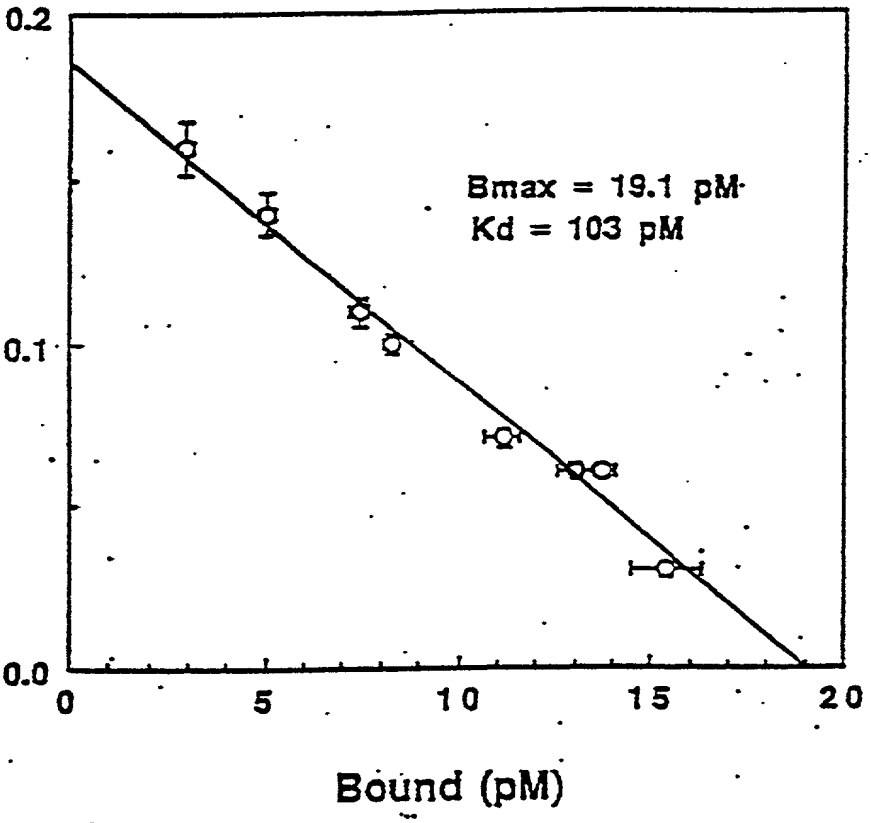
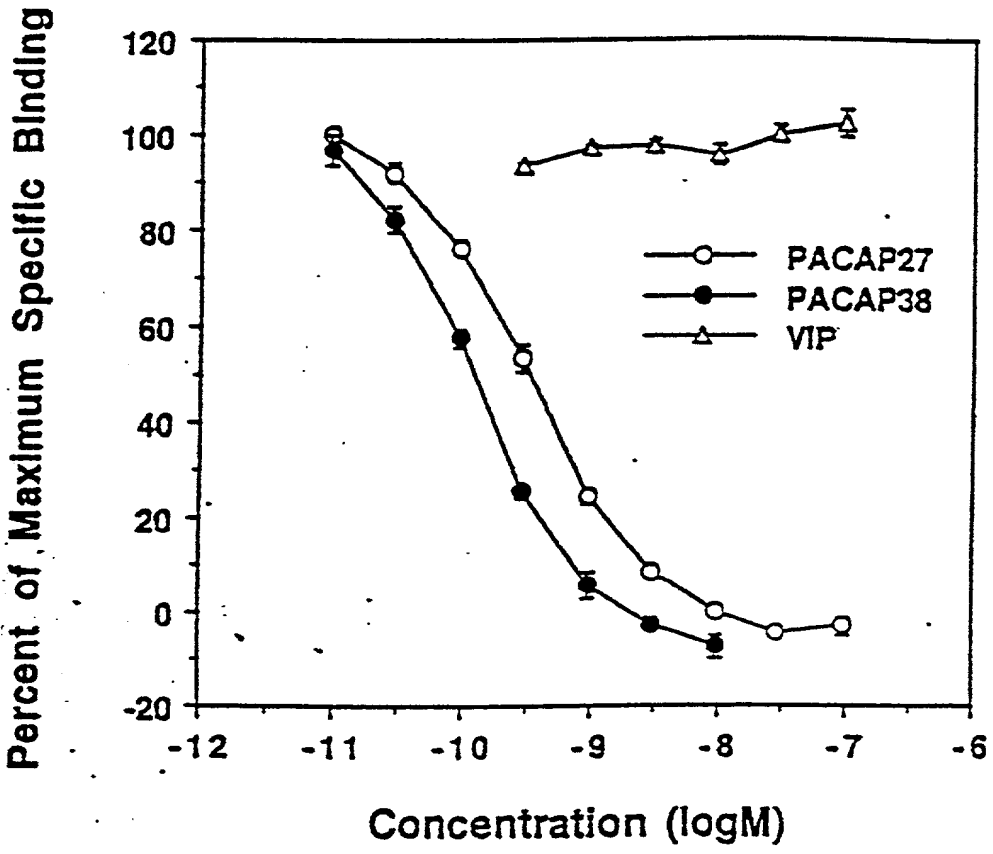


Fig. 35


Percent of Maximum Specific Binding
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100
80
60
40
20
0
-20
-12
-11
-10
-9
-8
-7
-6
PACAP27
PACAP38
VIP
Concentration (logM)

Fig. 36

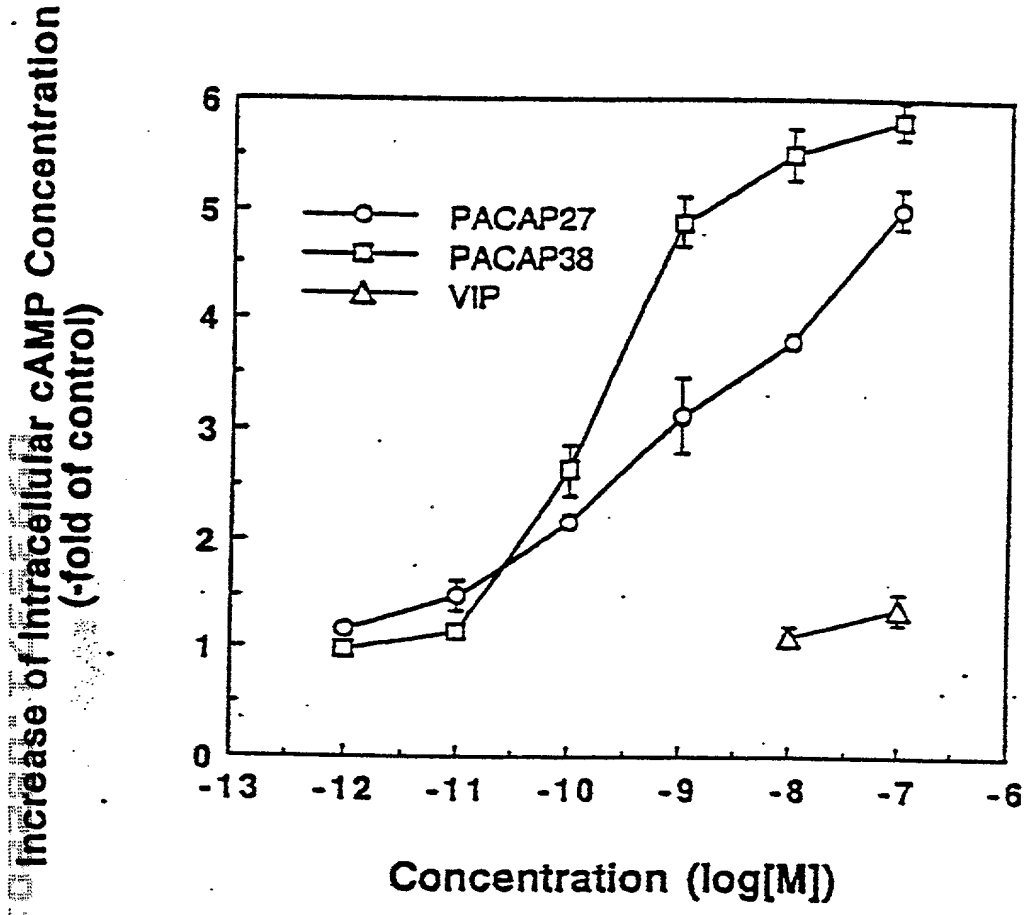

Increase of Intracellular cAMP Concentration
(-fold of control)
6
5
4
3
2
1
0
PACAP27
PACAP38
VIP
-13
-12
-11
-10
-9
-8
-7
-6
Concentration (log[M])

Fig. 37

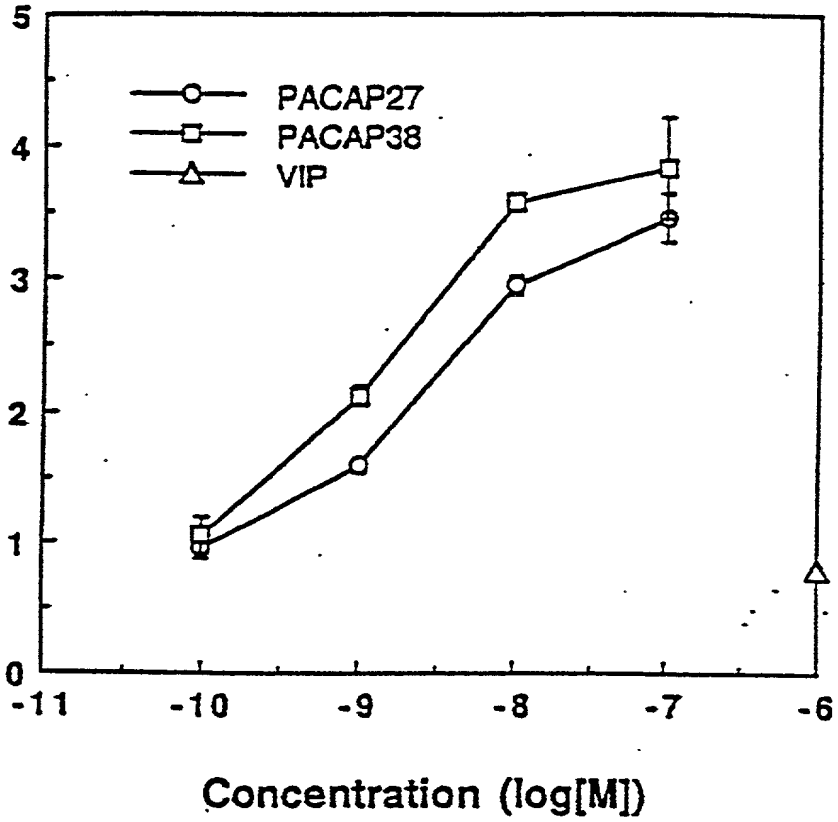

PACAP27
PACAP38
VIP
Accumulation of Inositolphosphates (-fold of control)
0
1
2
3
4
5
-11
-10
-9
-8
-7
-6
Concentration (log[M])

Fig. 38

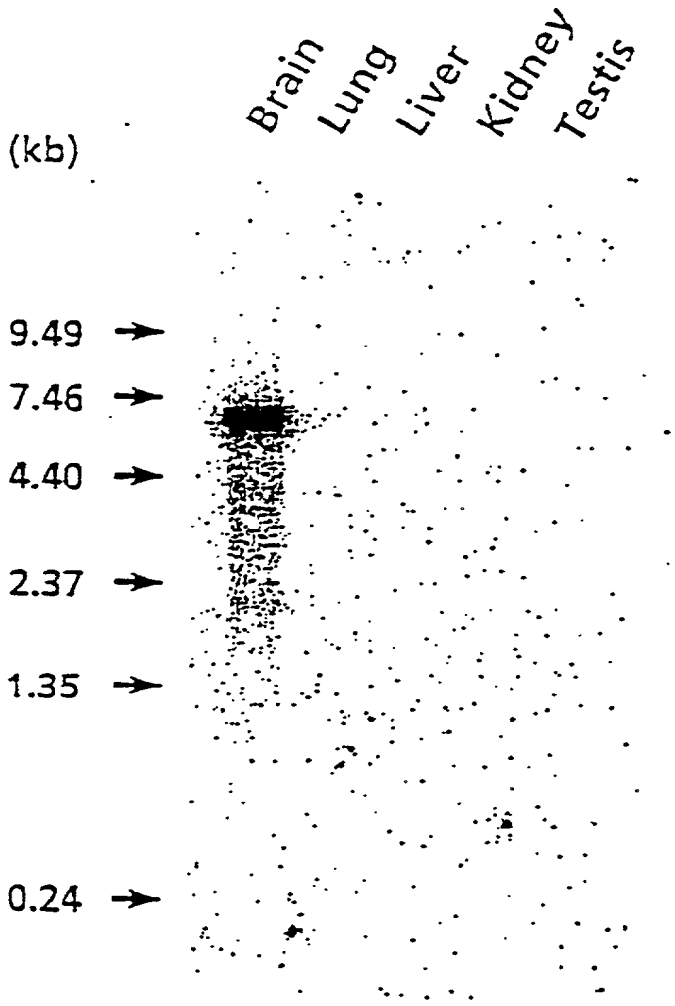
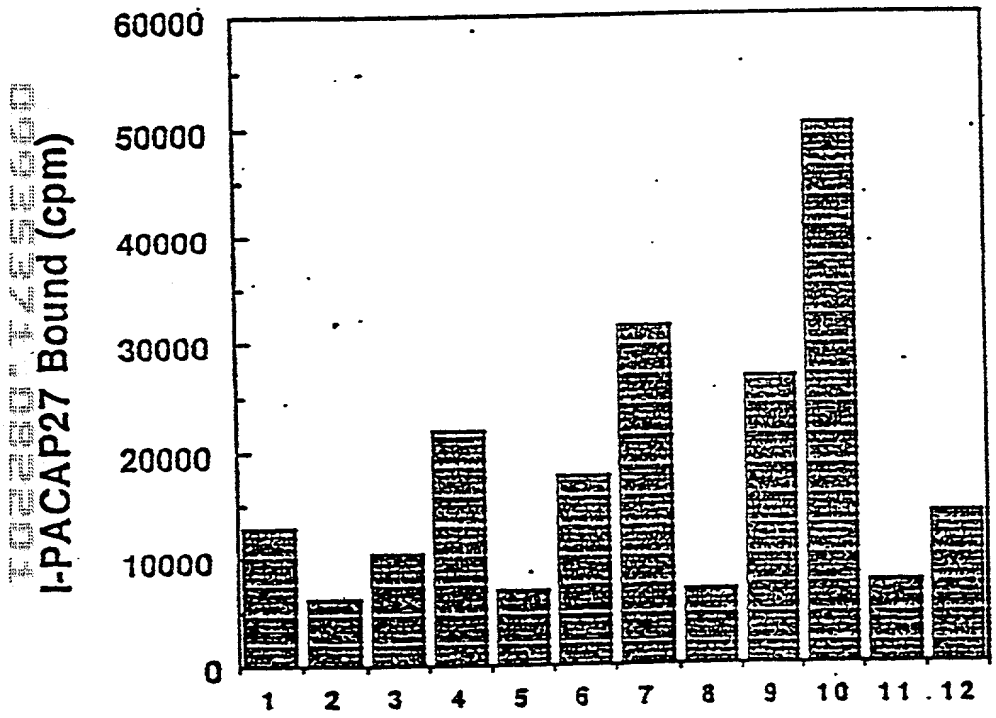


Fig. 39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50000
40000
30000
20000
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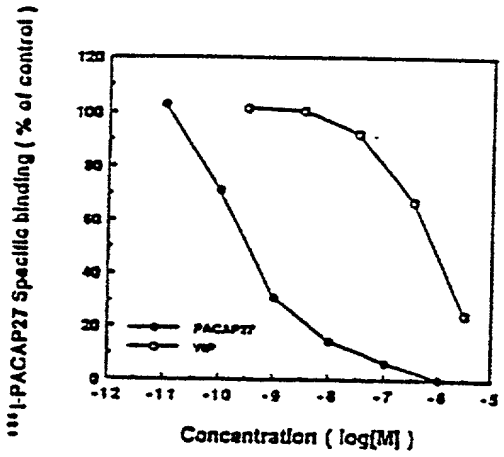
0
1
2
3
4
5
6
7
8
9
10
11
12

Fig. 40

A


^{125}I-PACAP27 Specific binding (% of control)
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
PACAP27
VIP
Concentration (log[M])

B

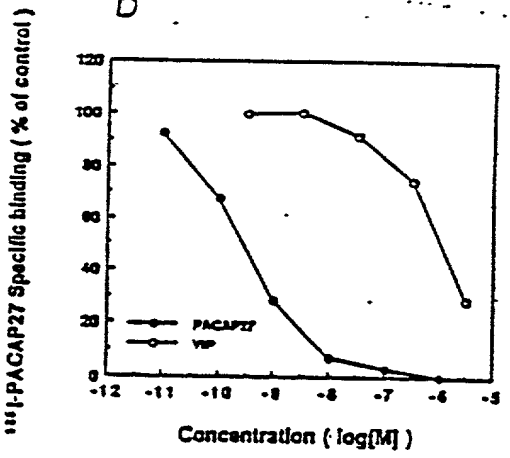

^{125}I-PACAP27 Specific binding (% of control)
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
PACAP27
VIP
Concentration (log[M])

Fig. 41

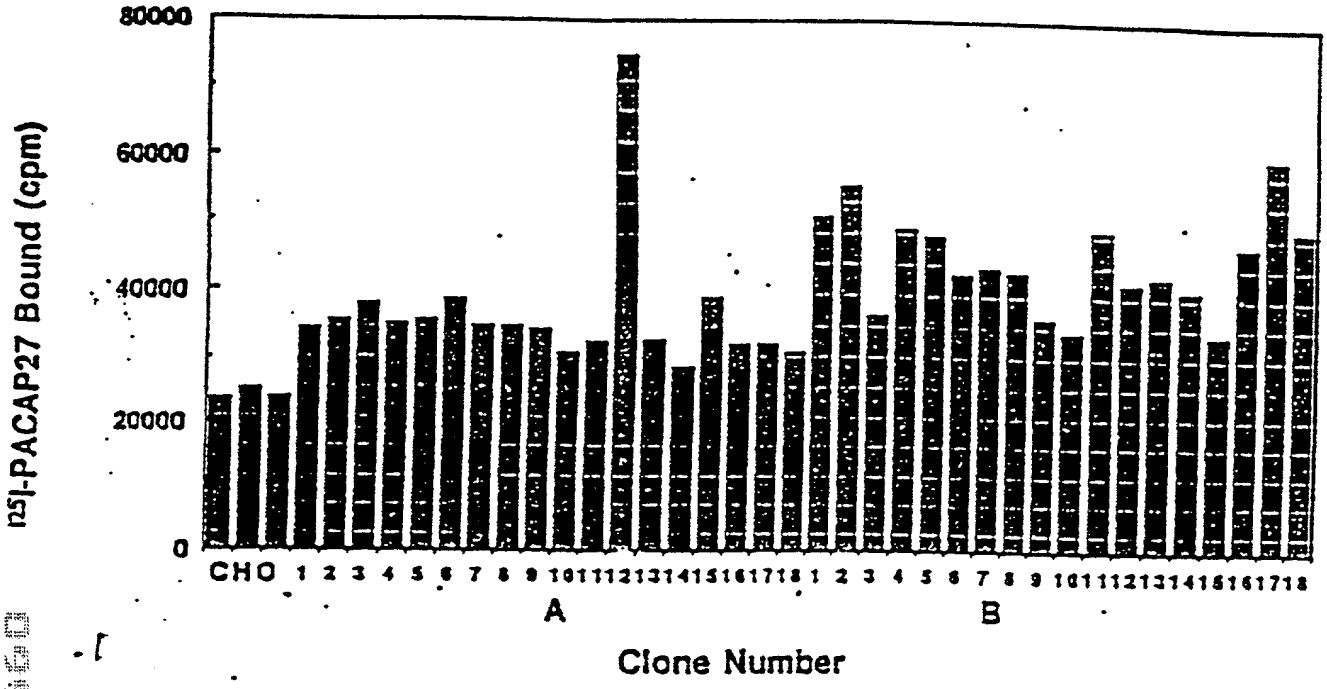

125I-PACAP27 Bound (cpm)
80000
60000
40000
20000
0
CHO 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
A
B
Clone Number

Fig. 42

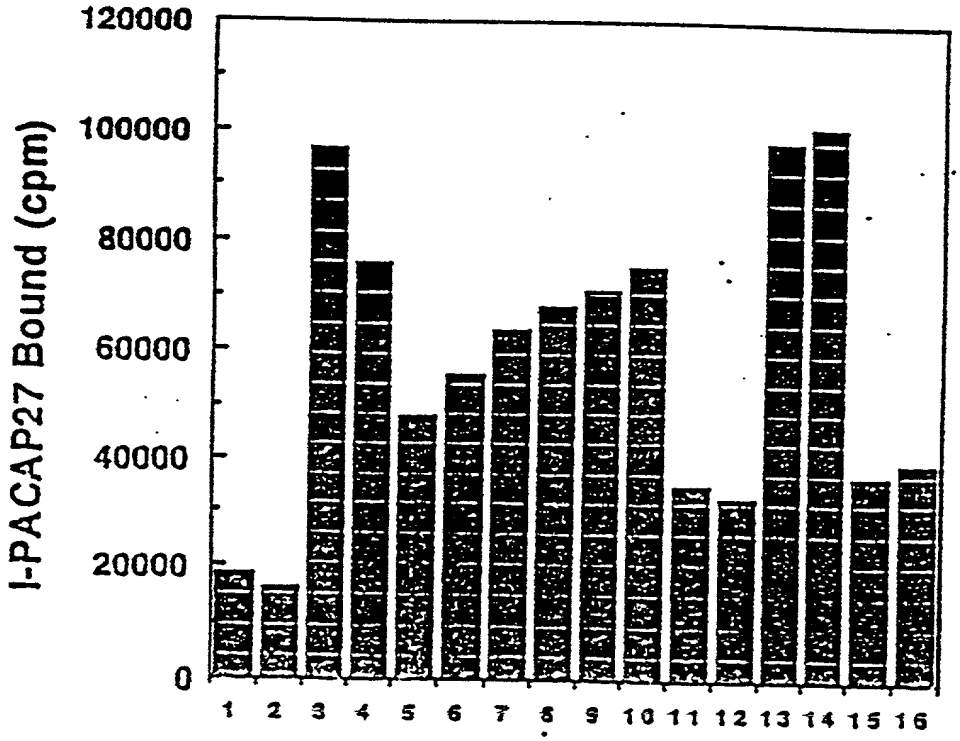
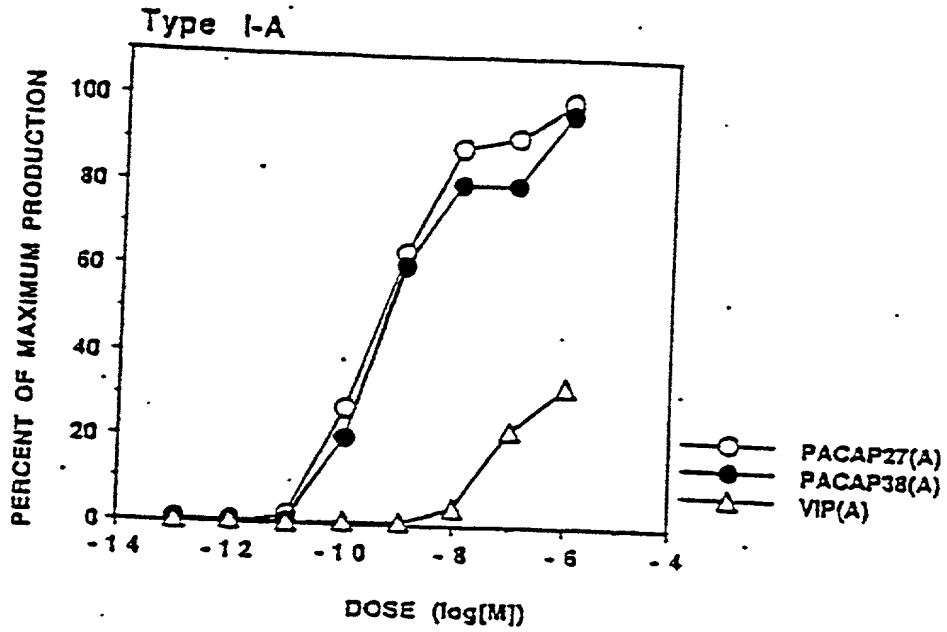

I-PACAP27 Bound (cpm)
120000
100000
80000
60000
40000
20000
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

Fig. 43

No. .....


Type I-A
PERCENT OF MAXIMUM PRODUCTION
100
80
60
40
20
0
-14
-12
-10
-8
-6
-4
DOSE (log[M])
PACAP27(A)
PACAP38(A)
VIP(A)

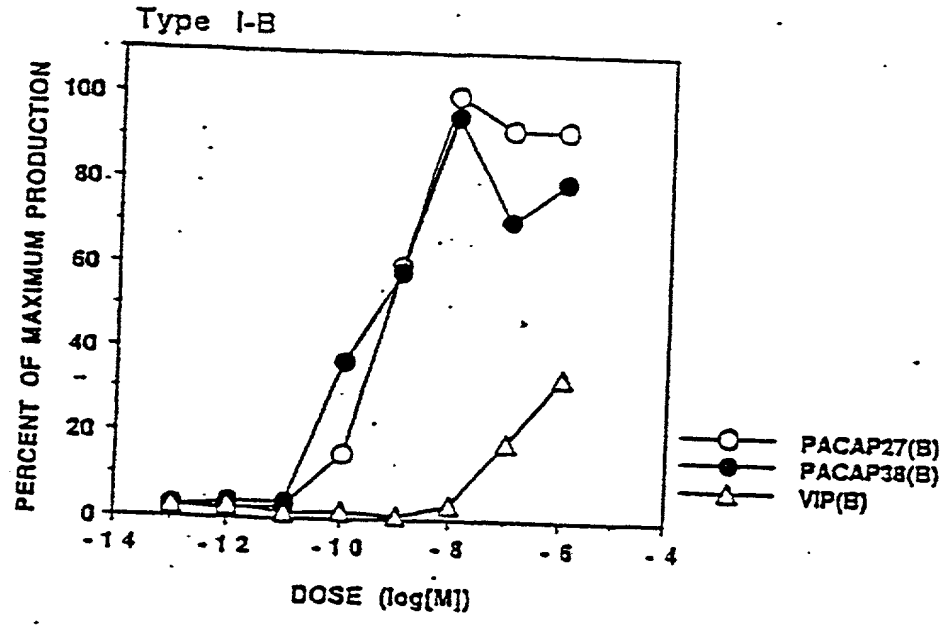

Type I-B
PERCENT OF MAXIMUM PRODUCTION
100
80
60
40
20
0
-14
-12
-10
-8
-6
-4
DOSE (log[M])
PACAP27(B)
PACAP38(B)
VIP(B)

Fig. 44

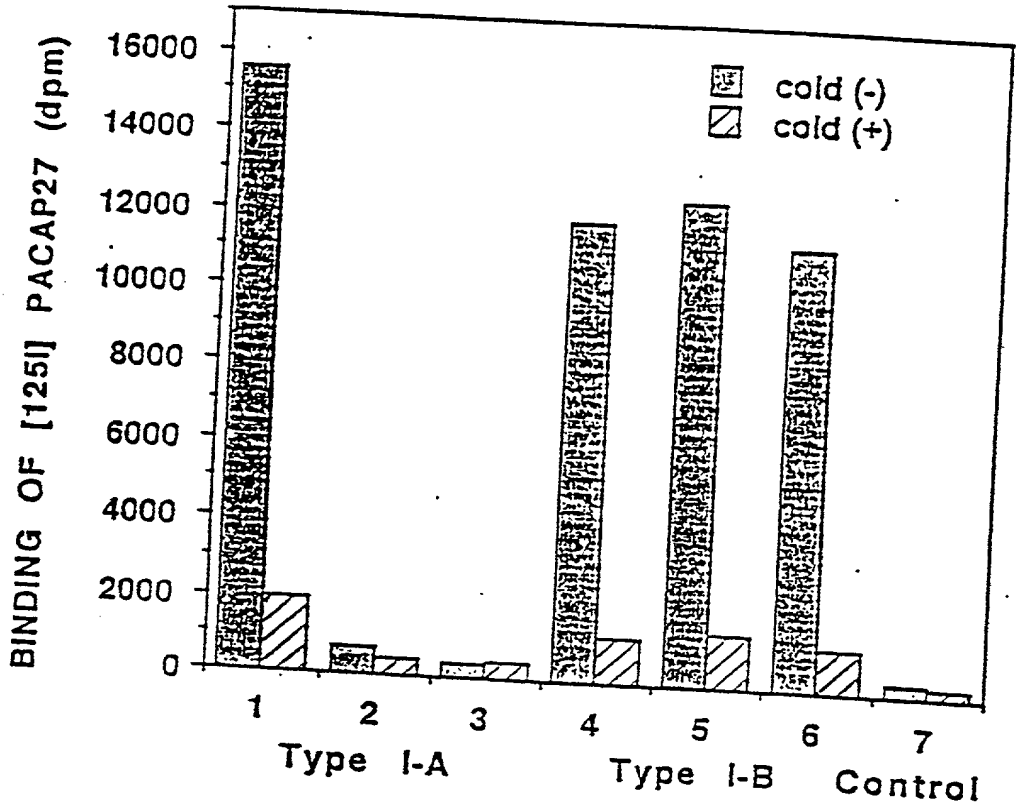
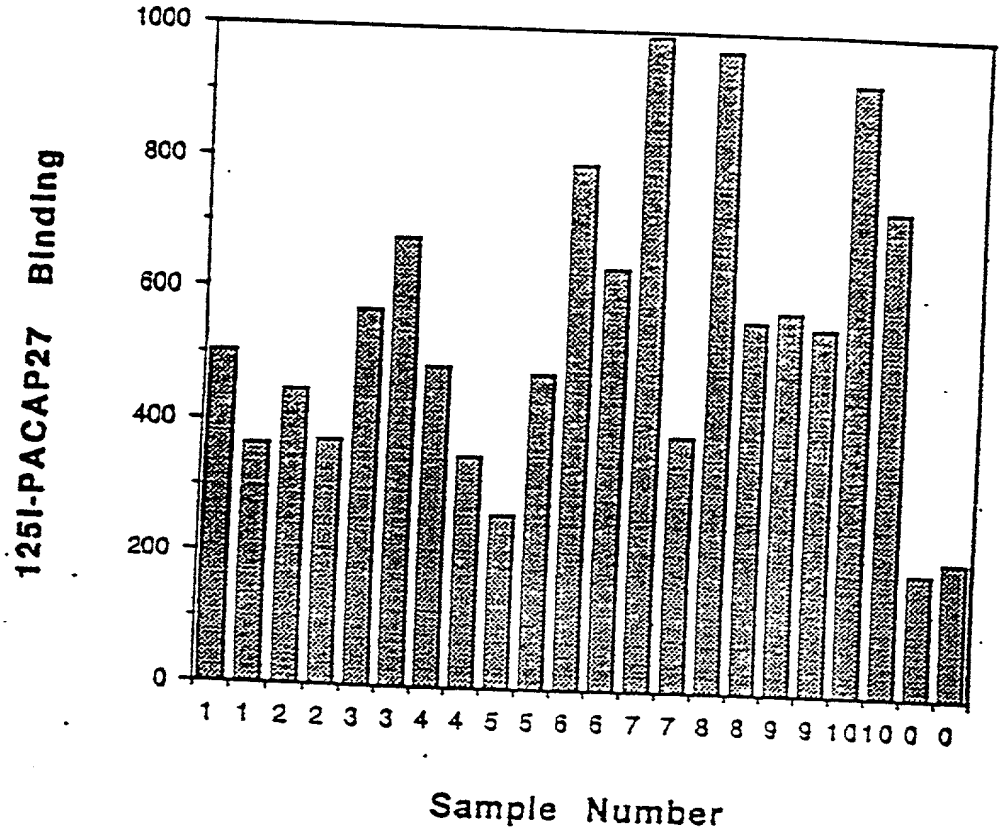
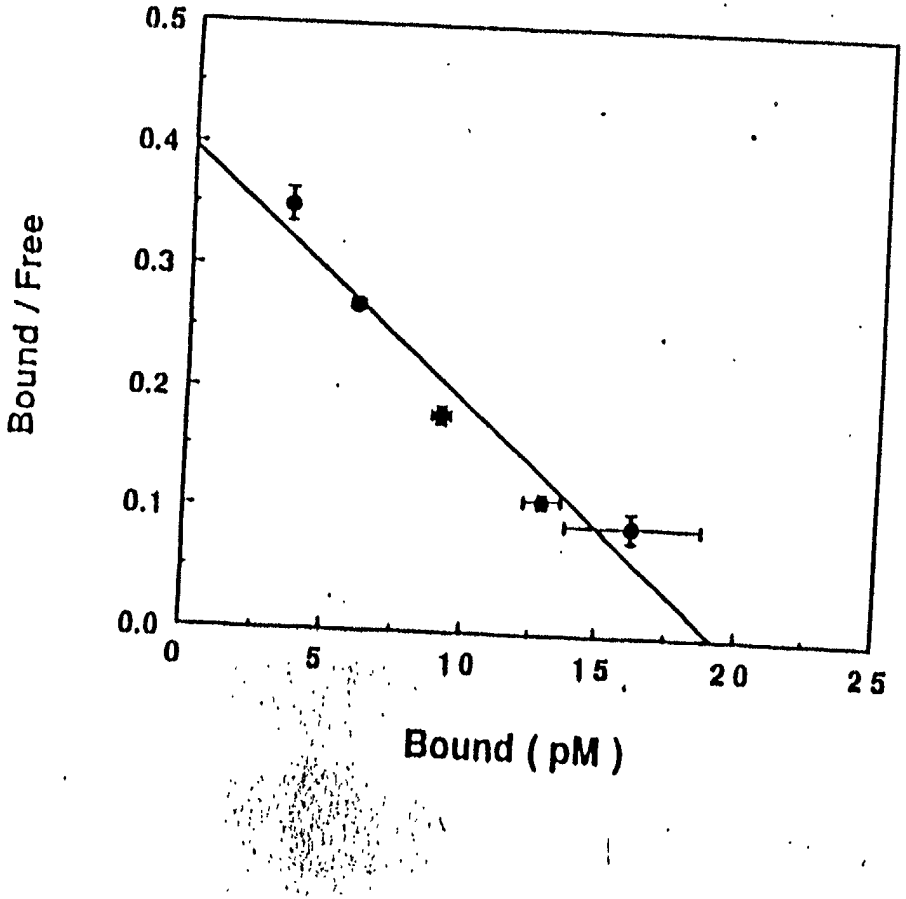

BINDING OF [125I] PACAP27 (dpm)
16000
14000
12000
10000
8000
6000
4000
2000
0
cold (-)
cold (+)
1
2
3
4
5
6
7
Type I-A
Type I-B
Control

Fig. 45


125I-PACAP27 Binding
1000
800
600
400
200
0
1 1 2 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10 0 0
Sample Number

A

Fig. 46



B

Fig. 47

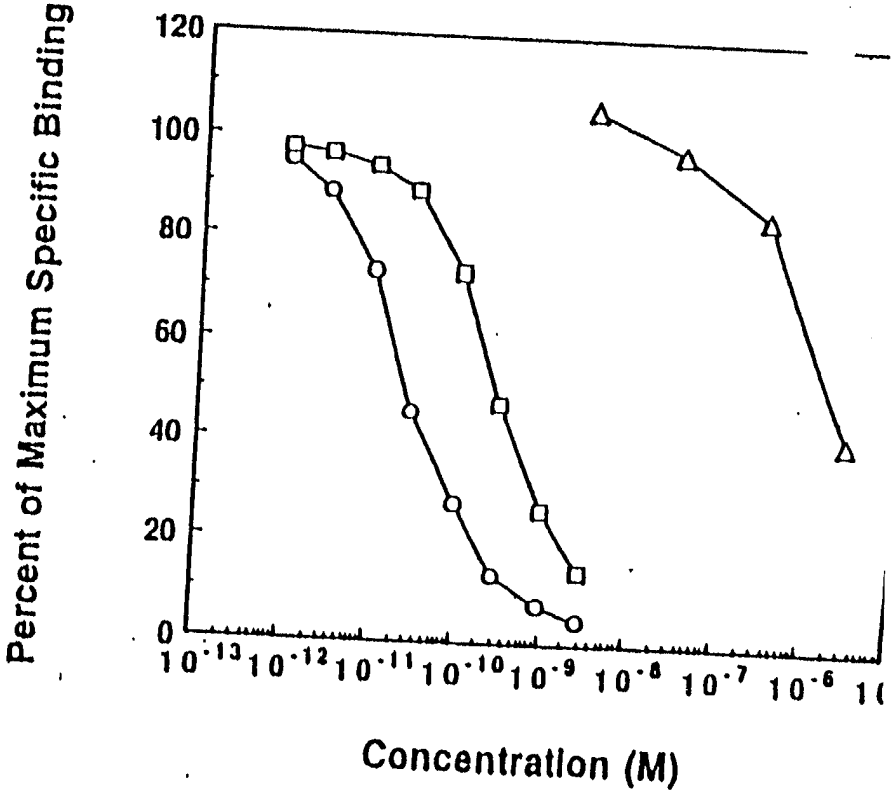


Fig. 48

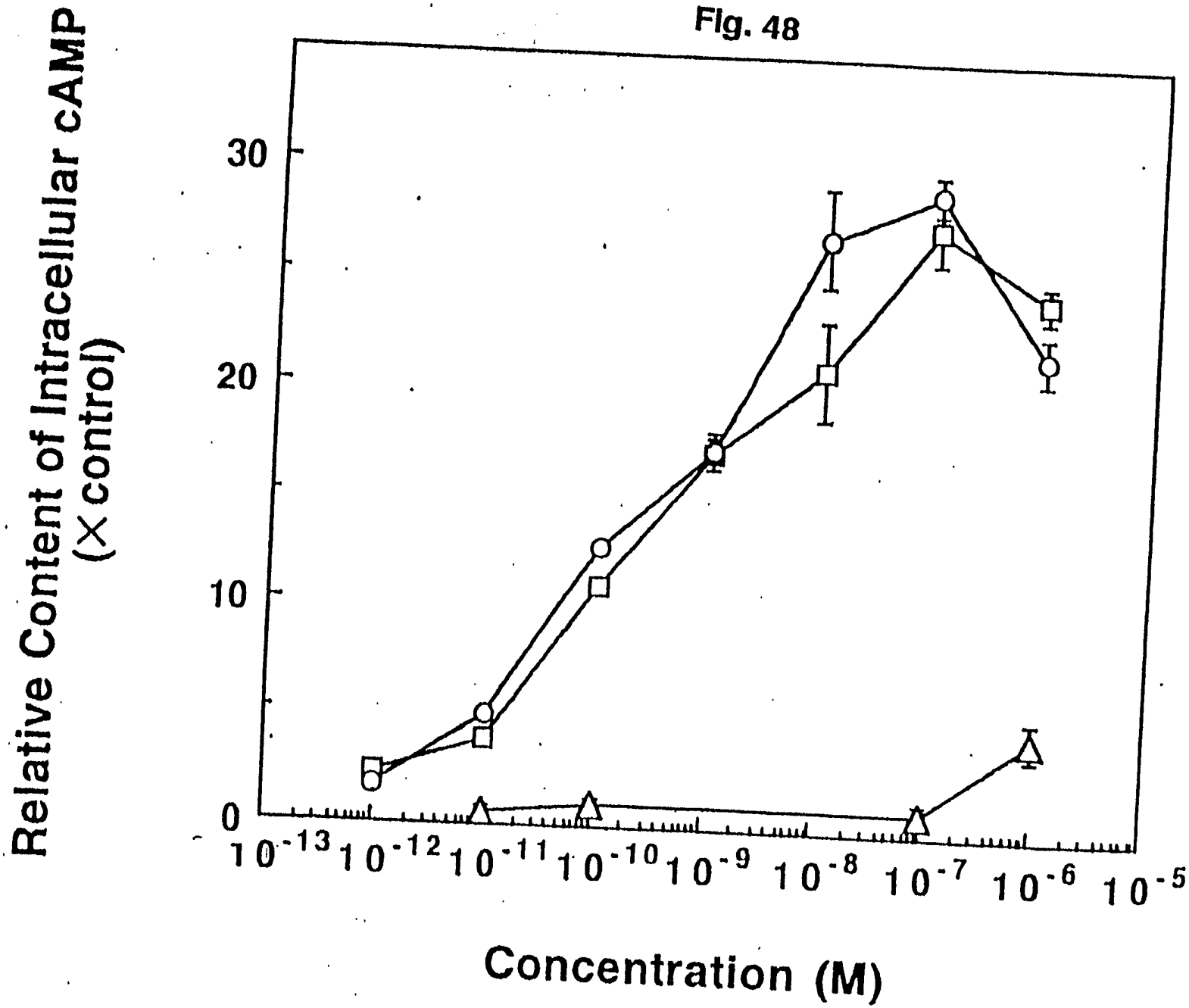

Relative Content of Intracellular cAMP
(× control)
30
20
10
0
10-13 10-12 10-11 10-10 10-9 10-8 10-7 10-6 10-5
Concentration (M)

Fig. 49

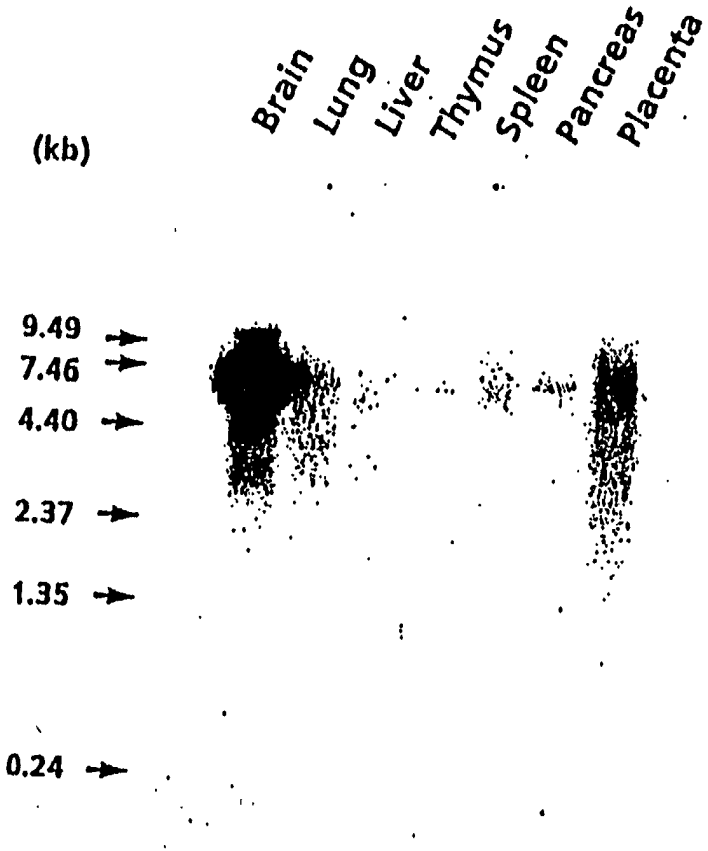
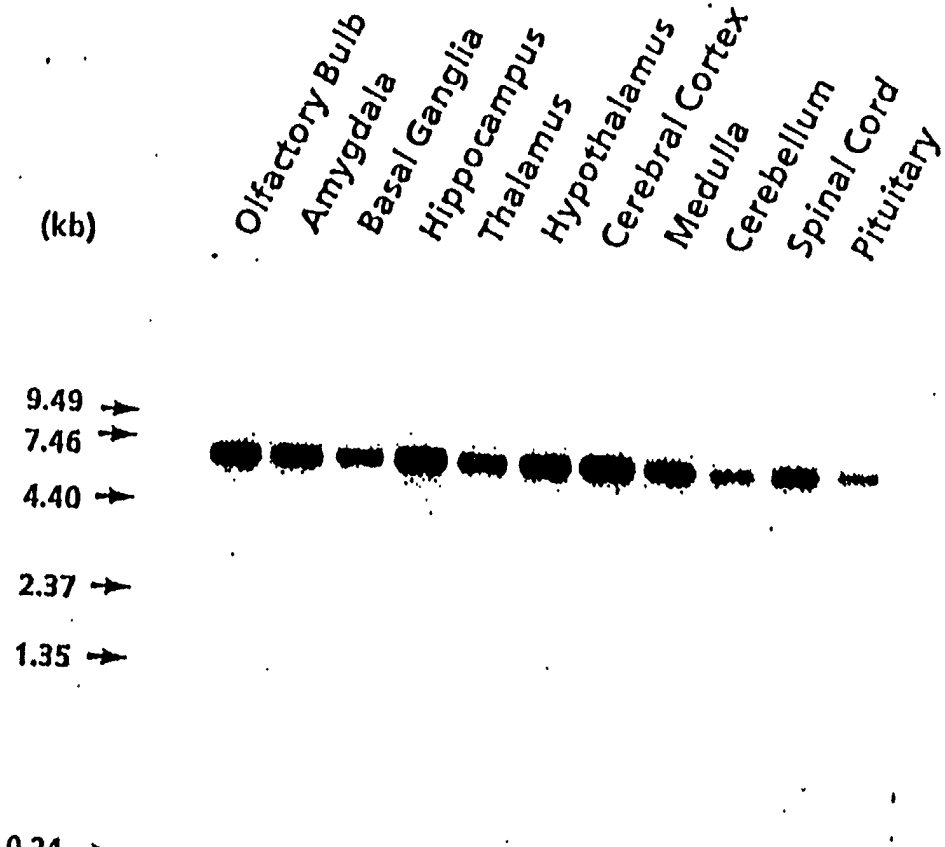
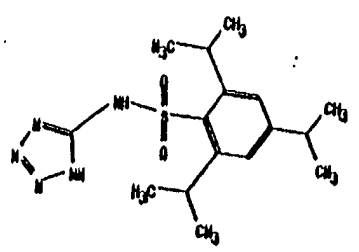

Brain
Lung
Liver
Thymus
Spleen
Pancreas
Placenta
(kb)
9.49
7.46
4.40
2.37
1.35
0.24

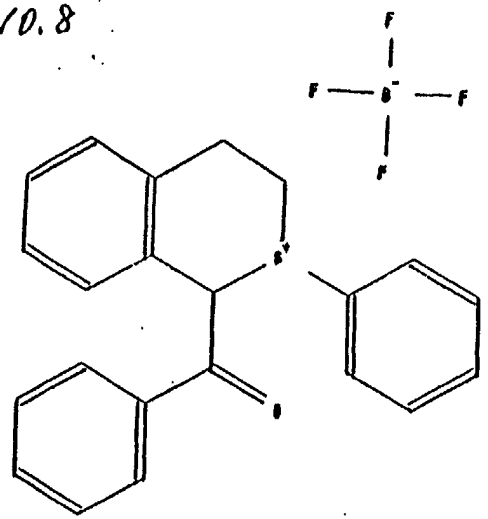
Fig. 50


Olfactory Bulb
Amygdala
Basal Ganglia
Hippocampus
Thalamus
Hypothalamus
Cerebral Cortex
Medulla
Cerebellum
Spinal Cord
Pituitary
(kb)
9.49
7.46
4.40
2.37
1.35
0.24

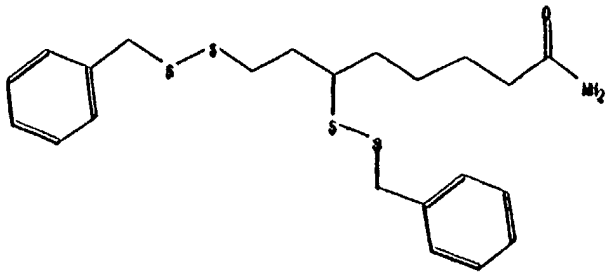
NO.7



NO.8



NO.9



NO.10

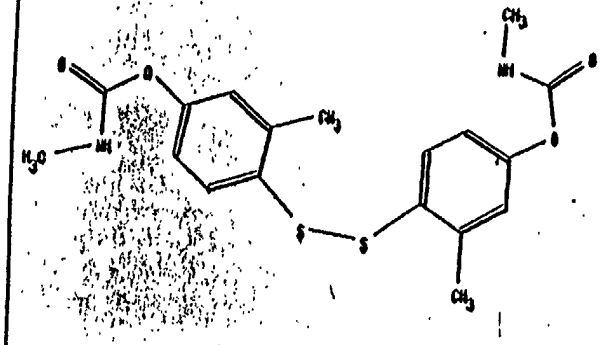
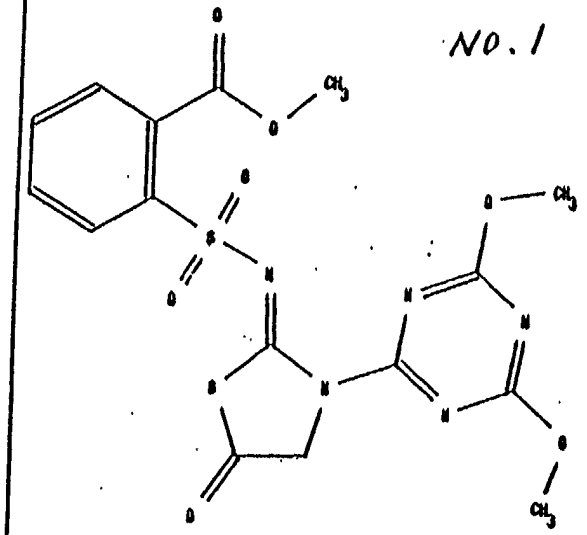
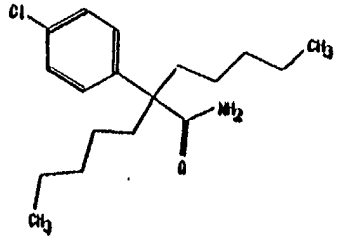


Fig. 51-2

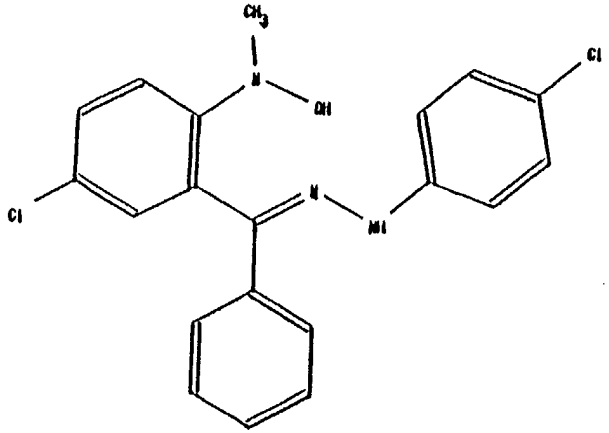
NO. 1



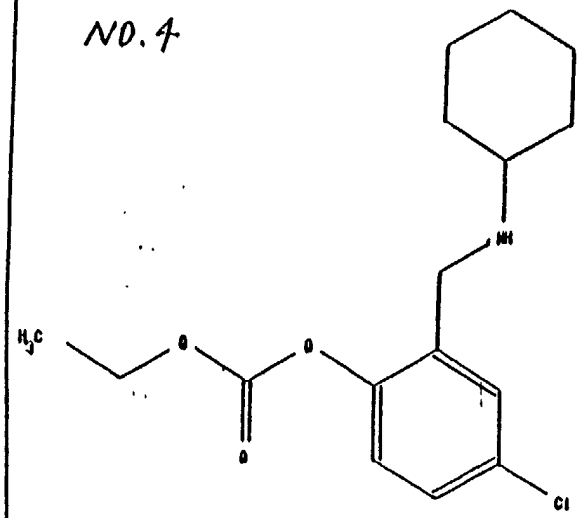
NO. 2



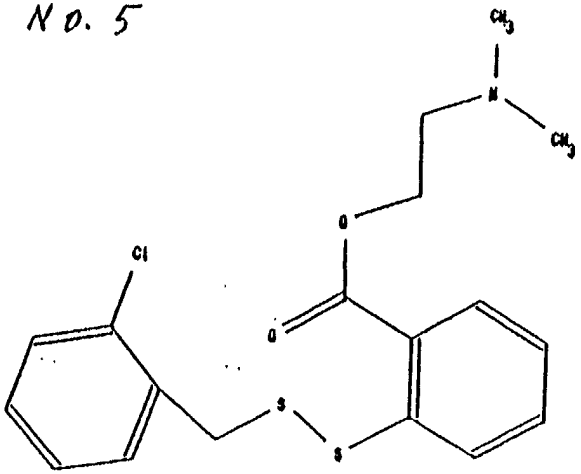
NO. 3



NO. 4



NO. 5



NO. 6

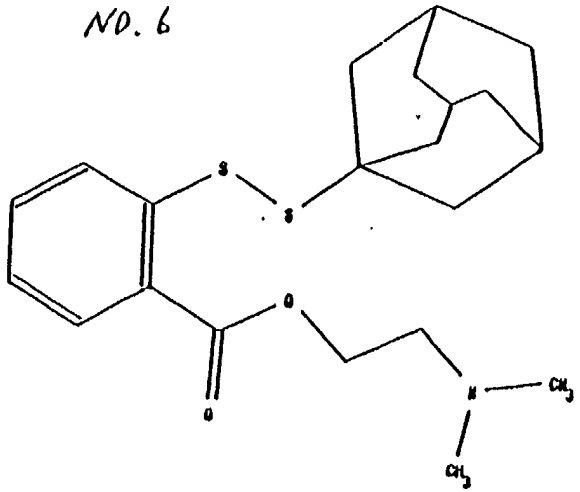


FIG. 1

Fig. 52

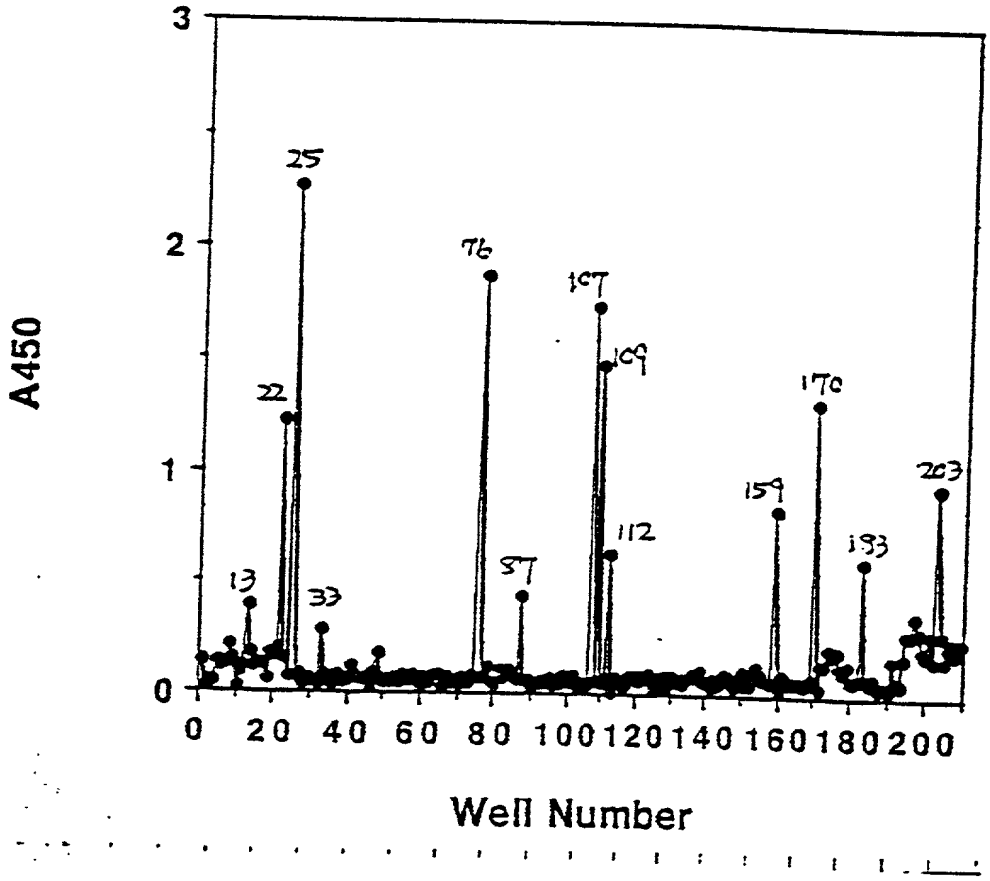

A450
3
2
1
0
25
22
13
33
76
57
107
109
112
159
170
193
203
0 20 40 60 80 100 120 140 160 180 200
Well Number

Fig. 53

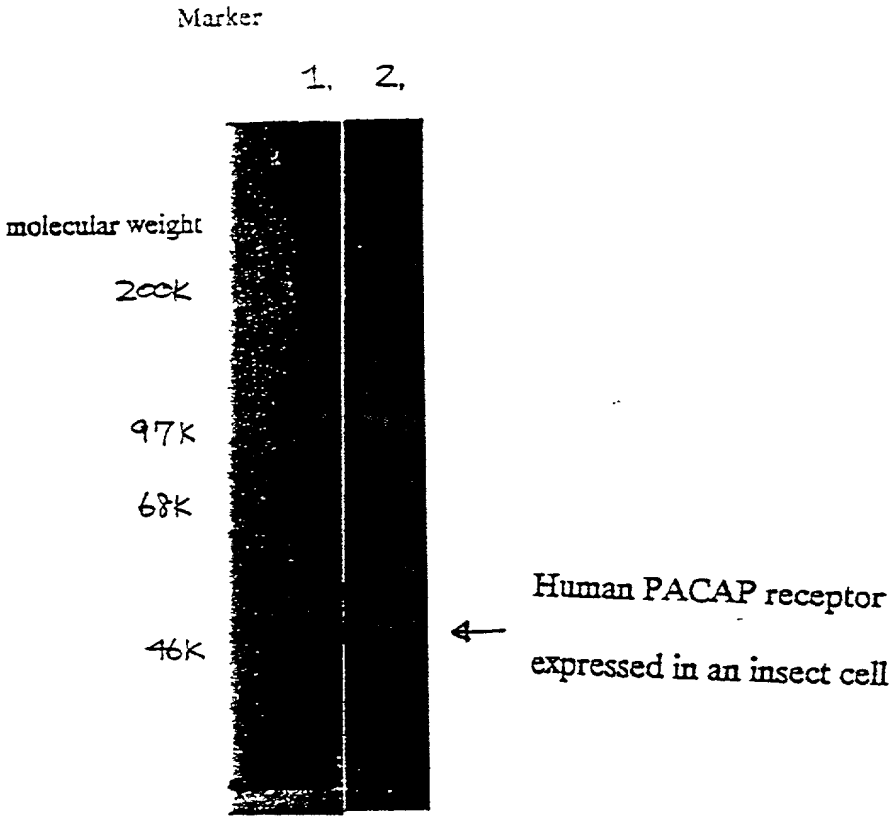
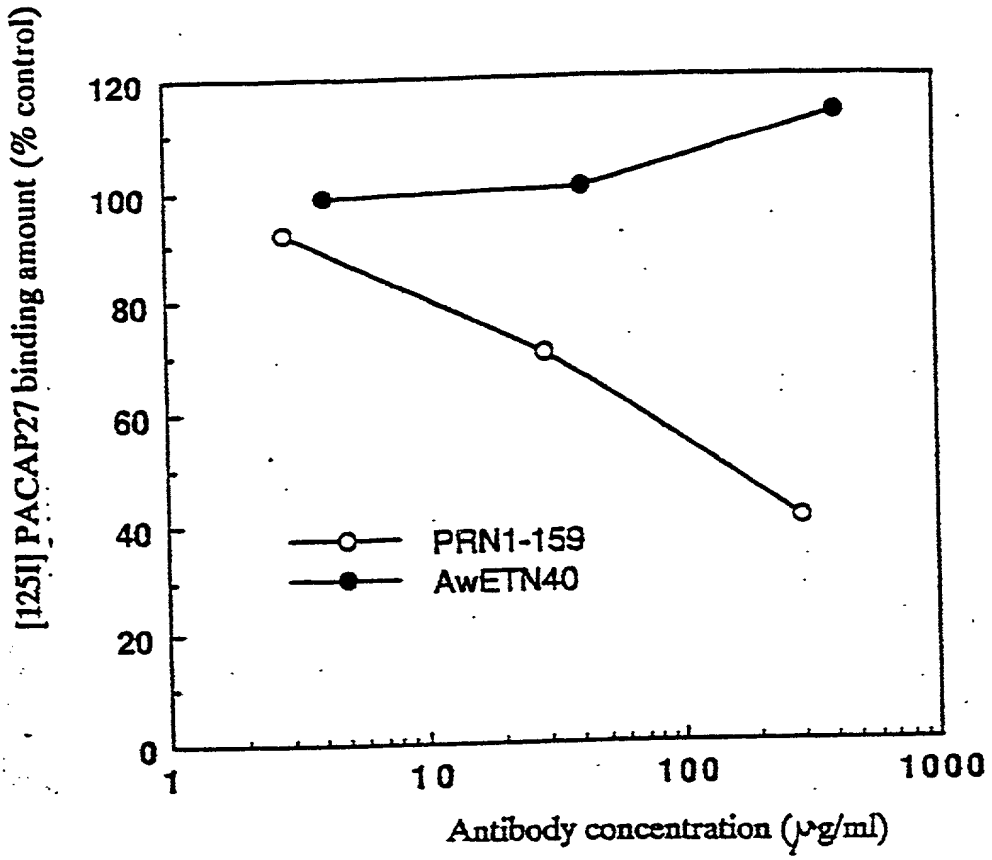

Marker
1.
2.
molecular weight
200K
97K
68K
46K
Human PACAP receptor
expressed in an insect cell

Fig. 54


[125I] PACAP27 binding amount (% control)
120
100
80
60
40
20
0
1
10
100
1000
PRN1-159
AwETN40
Antibody concentration (μg/ml)